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                  Copyright
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OM protein - protein search, using sw model

2, 2002, 12:15:08; Search time 17.4 Seconds (without alignments) 745.463 Million cell July Run on:

Title: Perfect score: Sequence:

US-09-810-506-2 1816 1 MAPEINTKLTVPVHSATGGE.....FIEALSEAGALQYVKA

PSAA 335

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.

SUMMARIES

Description	9r062 mus musc	P4697	15488 homo sap	3280 oryctol	08730 rattus	s 08960Ö	P47011 s	P36143	P25148	Q04545 saccha	P12916 human	P27129	Q58816 methano	P19816 salmon	P02242 eurype	P27480 phaseo	P37375 staphyloc	P23456 hantaan	P19817 salmone	Q9zs45	48658 hyoscy	060547	P28514 callip	P23606	P557	09x8h0 strepto	P27487 homo sap	P19239 mopeia	048660	Q96557 datura s	1107 bacter	5990d
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MEDLINE-99326495; PubMed-10395894;
Van Maanen M.-H., Fournier P.A., Palmer T.N., Abraham L.J.;
"Characterization of the human glycogenin-1 gene: identification muscle-specific regulatory domain.";
                                                                                                                      NLLETVKIVPPTLFAEQDFLNMYFK -----DIYKPIPPVYNLVLAMLWRHPENIEL-
                                                                                                                                                                                                                               VKVVHYCAAGAKPWRFTGEEE----NMDREDIKM-----LVKKWWDIYNDE---SLDY
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                             Length 332;
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM GN-1S).
TISSUE-Skin;
Leffers H., Wiemann S., Ansorge W.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
  CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Skeletal muscle;
TISSUE-Skeletal muscle;
MEDLINE-96176958; PubMed-8602861;
Barbetti F., Rocchi M., Bossolasco M., Cordera R., Finelli P., Consalez G.G.;
"The human skeletal muscle glycogenin gene: cDNA, and chromosomal localization.";
                                       -14;
137;
8DA0F1A875552F40
                            Score 243; DB 1;
Pred. No. 9.1e-14
); Mismatches 13
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                                                                                                                                                                                                                                                                                                                                        GLYG_HUMAN STANDARD; PRT; 349 AA. P46976; Q9UNVO; 01-NOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Glycogenin-1 (EC 2.4.1.186).
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PubMed=8661012;
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37271 MW;
                             13.4%;
25.1%;
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Genomics 33:519-522(1996)
                                               Conservative
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84; Conserv
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                             Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A. (ISOFORM GN-1L), AND ALTERNATIVE SPLICING.
MEDLINE=20184741; PubMed=10721716;
Zhai L., Mu J., Zong H., DePaoli-Roach A.A., Roach P.J.;
"Structure and chromosomal localization of the human glycogenin-2 gene GYG2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE.
PATHWAY: GLYCOGEN BIOSYNTHESIS.
SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; GN-1L (SHOWN HERE), GN-1 AND GN-1S; ARE PRODUCED BY ALTERNATIVE SPLICING.
PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10
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Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECHANISM,
FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRATE FOR
GLYCOGEN SYNTHASE.

-!- CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
                                                                                                                                                                                                                                                                                                                                                                                                                 THE PRESENCE OF
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O-LINKED (GLC. . .) (BY SIMILARITY)
MISSING (IN ISOFORM GN-1S).
MISSING (IN ISOFORM GN-1).
C41BCCFF54C8AF09 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESIDUES ATTACHED TO TYR-194.
SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 349;
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EMBL; U31525; AAB09752.1; -.
EMBL; X79537; CAA56073.1; ALT_FRAME.
EMBL; AF065481; AAD31084.1; -.
EMBL; AF065476; AAD31084.1; JOINED.
EMBL; AF065477; AAD31084.1; JOINED.
EMBL; AF065478; AAD31084.1; JOINED.
EMBL; AF065480; AAD31084.1; JOINED.
EMBL; AF087942; AAD52093.1; -.
EMBL; BC000033; AAH00033.1; -.
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SUBUNIT: HOMODIMER, TIGHTLY COMPLEXED TO GLYCOGEN SYNTHASE.
ALTERNATIVE PRODUCTS: AT LEAST 6 ISOFORMS; ALPHA (SHOWN HERE),
BETA, GAMMA, DELTA, EPSILON AND ZETA; ARE PRODUCED BY ALTERNATIVE
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  IEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF
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THAT SERVES AS SUBSTRATE FOR
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MEDLINE=20184741; PubMed=10721716;
Zhai L., Mu J., Zong H., DePaoli-Roach A.A., Roach P.J.;
"Structure and chromosomal localization of the human glycog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP
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015490; 015486; 015485; 015487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of human glycogenin-2, a initiator of liver glycogen metabolism."; J. Biol. Chem. 273:34850-34856(1998).
-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INFORM AN OLIGOSACCHARIDE PRIMER THAT SE
                                                                                                                                  -LSAAPDP-GWPDC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE TISSUE=Liver; MEDLINE=98010589; PubMed=9346895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosylglycogenin.
COFACTOR: SELF-GLUCOSYLATION IS
                                                                                                                                                                                        NLLETVKIVPPTLFAEQDFLNMYFK---
                                                                                                                                                                                                                                                                                   VKVVHYCAAGAKPWRFT -
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PANCKEAS. PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10

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TISSUE SPECIFICITY: EXPRESSED PREFERENTIALLY IN LIVER

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Y->F: LOSS OF ACTIVITY.
Y->F: NO LOSS OF ACTIVITY.
MISSING (IN REF. 1; AAB84378).
EKV -> AGI (IN REF. 1; AAB84376)
2EDE05FDAD5A7657 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 501;
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O-LINKED (GLC. . .).
MISSING (IN ISOFORM BETA).
MISSING (IN ISOFORM GAMMA).
MISSING (IN ISOFORM DELTA).
MISSING (IN ISOFORM EPSILON).
MISSING (IN ISOFORM ZETA).
V -> A.
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Alternative splicing
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          SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY
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U94364; AAB84378.1; -...
U94357; AAB84373.1; -...
U94357; AAB84373.1; -...
U94350; AAB84375.1; -...
U94361; AAB84375.1; -...
AF179615; AAF61855.1; JC
AF179616; AAF61855.1; JC
AF179619; AAF61855.1; JC
AF179620; AAF61855.1; JC
AF179620; AAF61855.1; JC
AF179621; AAF61855.1; JC
AF179622; AAF61855.1; JC
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228
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ACT_SITE 11
CARBOHYD 22
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                                                                                                                                                                                                                                                                                                              abbit skeletal muscle glycogenin. Molecular cloning and production fully functional protein in Escherichia coli.";
Biol. Chem. 267:25759-25763(1992).
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SUBSTRATE FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                liver glycogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lomako J., Whelan W.J.;
"The occurrence of serine phosphate in glycogenin: a possible regulatory wite ".
                                                                                                                                                                                                                                                                                                                                                                                                                        glycogenin
                                                                                                                                                                                                                                                                                        A.A.,
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
MEDLINE=93100288; PubMed=1281472;
Viskupic E., Cao Y., Zhang W., Cheng C., Depaoli-Roach
                                                                                                                                                                                               Vertebrata; Eule; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UDP
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INTER-SUBUNIT
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MEDLINE=99160387; PubMed=10049511;
Lin A., Mu J., Yang J., Roach P.J.;
"Self-glucosylation of glycogenin, the initiator of biosynthesis, involves an inter-subunit reaction.";
Arch. Biochem. Biophys. 363:163-170(1999).
-!- FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNI FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SU
                                                                                                                                                                                                                                                                                                                                                                                                                        muscle
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
STRAIN-NEW ZEALAND WHITE; TISSUE-Skeletal muscle;
MEDLINE-90032666; PubMed-2806254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                            34-47; 181-201; 209-226 AND 307-324
                                                                                                               01-JAN-1990 (Rel. 13, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycogenin-1 (EC 2.4.1.186).
GrG OR GYG1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.;
on rabbit
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CHARACTERIZATION.

MEDLINE=95289736; PubMed=7771798;

Cao Y., Steinrauf L.K., Roach P.J.;

"Mechanism of glycogenin self-glucosylation."

"Mechanism of glycogenin self-glucosylation."
                                                                                                                                                                                                                                                                                                                                                                                                                        skeletal
                                                                                                                                                                                               Craniata; Ve
1; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 34-47, AND PHOSPHORYLATION MEDLINE-89374676; Pubmed-3151442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYCOGEN SYNTHASE.
CATALYTIC ACTIVITY: UDP-glucose
glucosylglycogenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smythe C., Villar-Palasi C., Cohen "Structural and functional studies Eur. J. Biochem. 183:205-209(1989).
                                                                                                                                                                                                                                                                                                                                                                                                 Campbell D.G., Cohen P.;
"The amino acid sequence of rabbit The The Theorem 185:119-125(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89325337; Pubmed-2526735;
                                                                                                                                                                                 cuniculus (Rabbit).
Metazoa; Chordata; Ci
theria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory site.";
Biofactors 1:261-264(1988)
                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                   Roach P.J.;
"Rabbit skeletal muscle
                                                                                                                                                                                Oryctolagus cuniculu
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION. MEDLINE-94192798;
                                                                                                                                                                                                                          NCBI_TaxID=9986;
              SVQAGEA
NVVIGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF TISSUE-Liver
                                                                                       GLYG_RABIT
P13280;
                                                             GLYG_RABIT
300
                       297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
COFACTOR: SELF-GLUCOSYLATION IS DEPENDENT ON THE PRESENCE OF DIVALENT METAL IONS OF WHICH MANGANESE ION IS THE MOST EFFECTIVE. PATHWAY: GLYCOGEN BIOSYNTHESIS.
SUBUNIT: HOMODIMER TIGHTLY COMPLEXED TO THE 86 KDA CATALYTIC SUBUNIT OF GLYCOGEN SYNTHASE.
PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESIDUES FROM UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF AROUND 10 RESIDUES ATTACHED TO TYR-194.
SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACETYLATION.
PHOSPHORYLATION (BY CAPK) (IN VITRO).
O-LINKED (GLC. . .).
K->Q: LOSS OF ACTIVITY.
T -> L (IN REF. 4).
C -> S (IN REF. 2).
C -> L (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycogen biosynthesis; Acetylation; Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD64F6DE6CC5A8FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235.5; DB 1
Pred. No. 4.1e-13;
9; Mismatches 138
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LSAAPDP-GWPDC---
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85 K
38 T
88 C
97 C
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(Rel. 39, Last sequence)
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                 ; L01791; AAA31404.1; -. S06482; S06482.
A45094; A45094.
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008730;

30-MAY-2000

30-MAY-2000

16-OCT-2001
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MOD_RES
MOD_RES
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146
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                                                                                                                                         in
                                                       Rattus
                                                                                                                                                                                                                                                                   EFFECTIVE
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VD 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQL - - VDQGCVVKE
                                                                                                                                         glycogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -FNSGVFVYQPSIETYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLLHLASEQGSFDGGDQGLLNTYFSGWATTDITKHLPFVYNLSSLSIYSYLPAFKAFGKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycogen biosynthesis; Acetylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                    AROUND
                                         Craniata; Vertebrata; Euteleostomi
Sciurognathi; Muridae; Murinae; Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                       THE PRESENCE OF
                                                                                                                                                                                                                                                                                                             PALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JARITY)
                                                                                                                                                                                HANISM,
                                                                                                                                                                                                                                                                                                                                        DUES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332
                                                                                                                                                                Litted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: SELF-GLUCOSYLATES, VIA AN INTER-SUBUNIT MECH FORM AN OLIGOSACCHARIDE PRIMER THAT SERVES AS SUBSTRAT GLYCOGEN SYNTHASE (BY SIMILARITY).
CATALYTIC ACTIVITY: UDP-glucose + glycogenin = UDP +
                                                                                                                                                                                                                                                                                          PATHWAY: GLYCOGEN BIOSYNTHESIS.
SUBUNIT: HOMODIMER TIGHTLY COMPLEXED TO THE 86 KDA CAT
SUBUNIT OF GLYCOGEN SYNTHASE (BY SIMILARITY).
PTM: SELF-GLYCOSYLATED BY THE TRANSFER OF GLUCOSE RESI
UDP-GLUCOSE TO ITSELF, FORMING AN ALPHA-1,4-GLYCAN OF
RESIDUES ATTACHED TO TYR-194 (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
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                                                                                                                                       expression of rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (BY CAPK) SIMILARITY).
O-LINKED (GLC. . .) (BY S 41F19CA7F09BF059 CRC64;
                                                                                                                                                                                                                                                      DEPENDENT ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 231; DB 1
Pred. No. 1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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SIMILARITY
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                                                                                                                           S.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _transf_8
                                                                                                          STRAIN-WISTAR; TISSUE-Heart;
Pak B.J., Sangaralingham S.J., Pang 9
"Molecular cloning and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKVVHYCAAGAKPWRFTGEEENMDREDIKM-
                                                                                                                                                                                                                                    glucosylglycogenin.
COFACTOR: SELF-GLUCOSYLATION IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY
BY
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                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF021343; AAB81219.1; -
EMBL; U96130; AAB53334.1; -.
InterPro; IPR002495; Glycosyl-
Pfam; PF01501; Glyco_transf_8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37247 MW;
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25.1%;
2.4.1.186)
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74; Conserv
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                                                                                                FROM N.A
Glycogenin-1 (EC
                                                                   NCBI_TaxID=10116
                                                                                                                                                     cardiac tissue."
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43
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           OR GYG1.
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                                                                                               SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VYPPENQTEFAMAYYVINYS 102
                                                                                                                                                                                                                                                                                                                       Walsh S.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -EAKLGPKPPLYFNAGMFVYEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TKPDDDTVYHFNEDFKEYGASRSEFYPYLLAAVSDRGEHHSIPPEDTPYFNAGLMLIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLSTYHNLLETVKIVPPTLF----AEQDFLNMYFK-DIYKP---IPPVYNLVLAMLWRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SELHFNRILKIGRF--PYMYENAKMMEQSLLNLAFSLDGWFPWTRLDPYYNGV----W--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                a
   -YNPQTKSVKCESQDPIVSHPEFLNLWWDTFTTNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 371;
                                                                                                                                                                                                                                                                                                    STRAIN=972;
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A.,
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO S.POMBE SPBC4C3.08 AND SPBC4C3.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                   \boldsymbol{\mathsf{H}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               890BAD4A0E66379B CRC64;
                                                                                                                                                                 in chromosome
                                                                                                                                                               Hypothetical 43.7 kDa protein C5H10.12C in chromoson SPAC5H10.12C. SPAC5H10.12C. Schizosaccharomyces pombe (Fission yeast). Schizosaccharomycetes Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaes Schizosaccharomycetales; Schizosaccharomycetaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , DB 1;
6.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glycogen synthesis initiator protein GLG2.
GLG2 OR YJL137C OR J0663.
                                                                                                                                                 update)
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                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 6.20
Mismatches
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                                                                                                                                  Last sequence updarast annotation upprotein C5H10.12C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 165;
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Hypothetical protein; Transmembrane
TRANSMEM 17 33 POTENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43688 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sh 9.1%;
Similarity 25.0%;
67; Conservative 39
                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                 11-NOV-1995 (Rel. 32, C
11-NOV-1995 (Rel. 32, I
6-OCT-2001 (Rel. 40, I
(ypothetical 43.7 kDa p
207 AKVVHFLGR-TKPWNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324 PSIDERPLLKTAH---
                                                                                                                                                                                                                                         Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQCPDKVT
                                                                                                               01-NOV-1995
01-NOV-1995
16-OCT-2001
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P47011;
                                                                                      YAOC_SCHPO
Q09680;
                                                                                                                                                                                                                                                                                         SEQUENCE
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MEDLINE=96069371; PubMed=8524228;
Cheng C., Mu J., Farkas I., Huang D., Goebl M.G., Roach P.J.;
Requirement of the self-glucosylating initiator proteins Glg1p and Glg2p for glycogen accumulation in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 15:6632-6640(1995).
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                       res;
                                                                                                                                                                                                             STRAIN=S288C / FY1679;

MEDLINE=96408771; PubMed=8813765;

Katsoulou C., Tzermia M., Tavernarakis N., Alexandraki D.;

T "Sequence analysis of a 40.7 kb segment from the left arm of year chromosome X reveals 14 known genes and 13 new open reading fram I ncluding homologues of genes clustered on the right arm of chromosome XI.";

Yeast 12:787-797(1996).

'Yeast 12:787-797(1996).
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                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacchasomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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32, Last sequence update)
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1; X87371; CAA60818.1;
1; Z49412; CAA89432.1;
1; S0003673; GLG2.
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Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SELF-GLUCOSYLATING INITIATOR OF GLYCOGEN SYNTHESIS.
AS A PRIMER FOR THE ELONGATION REACTION CATALYZED BY GLYCOGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E5422F6ACEDD9CDA CRC64;
                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE GLYCOGENIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 122; DB 1
Pred. No. 0.0063
6; Mismatches 1
 update)
15-JUL-1999 (Rel. 38, Last annotation updiglycogen synthesis initiator protein GLG1 GLG1 OR YKR058W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 KNILOSIYTKIVLVEPLNCQEESIOKNSENLALLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002495; Glycosyl_transf_
Pfam; PF01501; Glyco_transf_8; 1.
Glycogen biosynthesis.
SEQUENCE 618 AA; 69912 MW; E5422F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---MFNSGVMMLIPD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 GGEKRAYVTFLAGTGDYVKGVVGLAKGLRK-
                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96069371; PubMed=8524228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- KQQTLQQFIEALS 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.7%;
18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U25546; AAA91646.1; -. EMBL; Z28283; CAA82136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 139-480 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S38134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ne EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERASE (RFAI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antelmann H., Bernhardt J., Schmid R., Hecker M.;

Antelmann H., Bernhardt J., Schmid R., Hecker M.;

"A gene at 333 degrees on the Bacillus subtilis chromosome encodes the newly identified sigma B-dependent general stress protein GspA.";

J. Bacteriol. 177:3540-3545(1995).

-!- INDUCTION: BY DIFFERENT STRESSES SUCH AS HEAT SHOCK AND SALT STRESS AND BY STARVATION.

-!- SIMILARITY: TO H.INFLUENZAE HI0259.

-!- SIMILARITY: TO LIPOPOLYSACCHARIDE 1,3-GALACTOSYLTRANSFERASE (RFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s reveals
                                                                                                                                                                                                                                                                                                              sacs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moszer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vertes A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND TO LIPOPOLYSACCHARIDE 1, 2-GLUCOSYLTRANSFERASE (RFAJ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           "A gene encoding a tyrosine tRNA synthetase is located near Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95020537; PubMed=7934828; Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Mosz Presecan E., Santana M., Schneider E., Schweizer J., Verte Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning and sequencing kb region from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                          MEDLINE=92216127; PubMed=1806041;
Glaser P., Kunst F., Debarbouille M., Vertes A., Danchin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2116367;
Cosgwell P., Chen K., Aymerich
                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
                                                 (Rel. 22, Created)
(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X52480; CAA36721.1; ALT_INIT.

EMBL; X73124; CAA51568.1; -.

EMBL; M2933; AAA75337.1; -.

EMBL; Z99123; CAB15869.1; -.

PIR; S16423; S16423.

Subtilist; BG10558; gspA.

InterPro; IPR002495; Glycosyl_transf_8.

Pfam; PF01501; Glyco_transf_8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the presence of the sacs locus the presence of two regulatory genes."; Gene 90:153-155(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF 1-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND SEQUENCE OF Pubmed=7768864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=QB1072;
MEDLINE=90337338; PubMed=2116367
Zukowski M.M., Miller L., Cosgwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 110-286 FROM N.A.
                                                                                                     protein A.
                                                                                                                                                                                                                                                                                                                                             DNA Seq. 1:251-261(1991).
                   STANDARD;
                                                                                                                                     Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERIZATION,
MEDLINE-95286551;
                                                                                                                                                                                                                          FROM N.A.
                                                                                                    General stress
GSPA OR IPA-12D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steinmetz M.;
                                                                                                                                                                                                                                                             MEDLL...
Glaser P., Ku
                                                 01-MAY-1992
01-FEB-1995
16-OCT-2001
                  GSPA_BACSU
P25148;
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=168;
                                                                                                                                                                                                                        SEQUENCE FR
STRAIN=168;
GSPA_BACSU
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                                                                                                                                           13;
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intergenic
                                                                                                                                                                                                        47 IKPDNKKRLEETTLKFGVPIEFLE---VDTNMYEHAVESSHITKAAYYRISIPDLIKDES
                                                                                                                                                                            -AYYVINYSKLRIWEF
                                                                                                                                                                                                                                               110 VEYNKMIYLDGDIQVFDNIDHLFDLPNGQF - - YAVMDCFCEKTWSHSPQYKIGYCQQCPD
                                                                                                                                                                                                                                                                                  -GQHERLKE
                                                                                                                                                                                                                                                                                                                   --PPTLFA---EQDF
                                                                                                                                                                                                                                                                                                                                                     148 MNVIDTGK-----YFNSGIMIIDFESWRKQNITE--KVINFINEHPDEDFLVLHDQDA
                                                                                                                                                                                                                                                                                                                                                                                       -- AMLWRHPENIELDQVKVVHYCAAGAKPWRF
                                                                                                                                                                                                                                                                                                                                                                                                                         199 LNAILYDOWYELHPRWNAQTYIMLKLKTPSTLLGRKQYNETRENPAIVHFC-GGEKPWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                        62;
                                                                                                       Length 286;
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUB1-CPR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wn D., Bowman S., Barrell B.G., Rajandream M.A.;
mitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: STRONG, TO YEAST ZMS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases
                 -> A (IN REF. 4).
-> V (IN REF. 4).
A282BE6E3B6518DE CRC64;
                                                                                                                                                                                                                                                                                                                   168 KVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIV---
                                                                                                                                        101;
                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YMII_YEAST STANDARD; PRT; 1251 AA. Q04545; Q03621; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical 141.5 kDa zinc finger protein in
                                                                                                                                                                                                                                                                                104 IK--RMIYIDCDALVLEDISKLWDLDIAPYTVAAVEDA--
                                                                                                      Score 110; DB
Pred. No. 0.027
39; Mismatches
                                                                                                                                                                          --GCVVKEIEPVYPPENQTEFAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                       219 LUMYFKDIYKPIPPVYN----LVL--
                                                                                                                                        39;
                    ပ အ
               12 C
27 S
33522 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 469-1251 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 TGEEENMDREDIKMLVKKWWDIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 NTKHPYRDEYFHYMSYTKWNTIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGD; S0004546; YML081W.
InterPro; IPR000822; Znf-C2H2
Pfam; PF00096; Zf-C2H2; 2.
PRINTS; PR00048; ZINCFINGER.
                                                                                                       6.1%;
23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z46660; CAA86657.1; -
EMBL; Z46373; CAA86497.1; -
HSSP; P07248; 1ARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-488 FROM N.A. STRAIN-S288C / AB972;
                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=S288C / AB972;
Brown D., Bowman S., I
Submitted (OCT-1994)
                                                                                                                                                                            VPEDHRKQLVDQ--
               12
27
286 AA;
                                                                                                                       Similarity
 proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                      62;
Complete
CONFLICT
CONFLICT
SEQUENCE
                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YML081W
                                                                                                                                                                            62
                                                                                                                                         Matches
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                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                       870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  976
                                                                                                                                                                                                                                                                                                         41 LAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVIN 100
                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLG_HRV1B STANDARD; PRT; 2157 AA.

POLG_HRV1B STANDARD; PRT; 2157 AA.

P12916; Q89704; Q82106; Q82107; Q82108; Q82110; Q82111;
Q82112; Q82113; Q82114; Q82115;
Q1-OCT-1989 (Rel. 12, Last sequence update)
O1-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Genome polyprotein [Contains: Coat proteins VP1 TO VP4; Core proteins P2A TO P2C, P3A; Genome-linked protein VPG; Picornain 3C
(EC 3.4.22.28) (Protease 3C) (P3C); RNA-directed RNA polymerase P3D (EC 2.7.7.48)].

Human rhinovirus 1B (HRV-1B).

Viruses; SSRNA positive-strand viruses, no DNA stage; Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                  779 LVQLIKISKLNYPLENFIKPPIESDHVLEYQDNPAVLNQFKAQYNTREQINRNFKYFILA 838
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITS,
P1, VP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEINS
                                                        Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                     --HSIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - PWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEKCLMYLSNGNPYLYKNAKISFKTLLSLLISIHEKINIERDALKDSYESDFHAKNVQWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -- LFFCENSRTWNENLTRFNIVLDSKFSLIEVSNGESN
                                                                                                                                                                                                                                                                                                                                                                                             YSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMD---CFCEKTWSHSPQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes P.J., North C., Jellis C.H., Minor P.D., Stanway G.;
"The nucleotide sequence of human rhinovirus 1B: molecular
relationships within the rhinovirus genus.";
J. Gen. Virol. 69:49-58(1988).

-!- FUNCTION: P3C POLYPEPTIDE IS A PROTEASE THAT CLEAVES AT CERT
Q/G SITES IN THE POLYPROTEIN. IT MAY BE A CYSTEINE PROTEASE.

-!- SUBUNIT: THE VIRUS CAPSID IS COMPOSED OF 60 ICOSAHEDRAL UNIT
EACH OF WHICH IS COMPOSED OF ONE COPY EACH OF PROTEINS VPI,
                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLN - - MYFKD - - - - IYKPIPPVYNLVLAMLWRHPE - - NIELDQVKVVHYCAAGAK
                                                                                                                                                                                                                     Length 1251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PI
SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                   612F064177D6FF3B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        -HIVLLISNLFKSLVDFDCCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     977 M-----HSRPLVATMLKHWELLYIKNGGILALSDENLPIIN 1012
                                                                                                                                                                                                                                                            107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --NDESLDYKN
                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                     Score 105; DB Pred. No. 0.46;
                                                                                                                                                                                                                                         ed. No. 0.46
Mismatches
                         2 2
SMART; SM00355; ZnF_C2H2; 2.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2
Hypothetical protein; Nuclear protein; DNA-binding; Repeat.
                                                                                                              C2H2-TYPE
                                                                                                                                C2H2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=88089537; PubMed=2826669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 FTGEEENMDREDIKMLVKKWWDIY----
                                                                                                                                                    141464 MW;
                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                    5.8%;
llarity 20.6%;
Conservative 4
                                                                                                          83
112
                                                                                                                                                   1251 AA;
                                                                                                                                                                                                                                        Similarity
58; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCGV - - PCYNEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        839 OSRIRIC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhinovirus
                                                                                                                              ZN_FING
SEQUENCE
                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                              ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
POLG_HRV1B
                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              871
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                                        DR
KW
FT
SQ
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                                                                                                                 InterPro; IPRu., PF00226; Pico_P2A; 1. Pfam; PF00152; Pico_P2B; 1. Pfam; PF00103; rhv; 3. R ProDom; PD001125; Cys-protease-3C; 1. DR ProDom; PD001126; Cys-protease-3C; 1. DR ProDom; PD001126; Cys-protease-3C; 1. DR ProDom; PD001126; Cys-protease; 1. Coat procein; Coat procein; Coat protein; Transferase; KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; KW RNA-directed RNA polymerase; Hydrolase; Thiol protease; Coat PROTEIN VP2 (P1B). 333 570 COAT PROTEIN VP2 (P1B). 571 857 COAT PROTEIN P2C. CORE PROTEIN P2C. CORE PROTEIN P2C. CORE PROTEIN P3A. 1094 CORE PROTEIN P3A. TROME-LINKED PROTEIN VF "NAIN 3C. "TED RNA POLYME" "TAL).
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RNA-DIRECTED RNA POLYMERASE
MYRISTATE (BY SIMILARITY).
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PROTEASE (POTENTIAL).
W; 42DB649063B677B9 CRC64;
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Mismatches
                                                                                Cys-protease-3C
Pico_PlA.
EMBL; D00239; BAA00168.1; -.
PIR; A28699; GNNY1B.
HSSP; Q82122; 1AYN.
MEROPS; C03.007; -.
MEROPS; C03.021; -.
InterPro; IPR000199; Cys-protease-:
InterPro; IPR00013138; Pico_P1A.
InterPro; IPR000081; Pico_P2A.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001205; RNA_pol_P3D.
InterPro; IPR001676; RNV.
Pfam; PF00548; Cys-protease-3C; 1.
Pfam; PF00226; Pico_P1A; 1.
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the lipopolysaccharide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb:or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                    STRAIN=Ki2 / Mc1033;
MEDLINE=94316500; PubMed=8041620;
Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Bla
"Analysis of the Escherichia coli genome. V. DNA sequence
region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22:2576-2586(1994).
-!- CATALYTIC ACTIVITY: UDP-glucose + lipopolysaccharide =
glucosyl-lipopolysaccharide.
-!- PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.
-!- SIMILARITY: TO S.TYPHIMURIUM RFAJ AND TO RFAI.
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g as its content
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819428EA13F1959A CRC64;
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01-OCT-1992 (Rel. 23, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lipopolysaccharide 1,2-glucosyltransferase (ECREAJ OR WAAJ OR B3626.
Escherichia coli.
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                                                                                                                                                                        STRAIN=K12;
MEDLINE=92325066; PubMed=1624461;
Pradel E., Parker C.T., Schnaitman C.A.;
"Structures of the rfaB, rfaI, rfaJ, and
coli K-12 and their roles in assembly of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG11353; rfaJ.
InterPro; IPR002495; Glycosyl_transf_
Pfam; PF01501; Glyco_transf_8; 1.
Lipopolysaccharide biosynthesis; Glyc
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ene; EG11353; r
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                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
Science 273:1058-1073(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RESPONSIBLE FOR THE AMIDATION OF CARBOXYLIC GROUPS AT POSITION A AND C OF EITHER COBYRINIC ACID OR HYDROGENOBRYNIC ACID NH(2) GROUPS ARE PROVIDED BY GLUTAMINE, AND ONE MOLECULE OF ATP IS HYDROGENOLYZED FOR EACH AMIDATION (BY SIMILARITY). PATHWAY: COBALAMIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --GRHLGLVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LDKIVEIADEDFEEVDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 AKLGPKPPLYFNAGM-FVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE COBB/COBQ FAMILY. COBB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 443;
                                                                                                                                                                                                                                                                  Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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InterPro; IPR002586; CbiA.
Pfam; PF01656; CbiA; 1.
Cobalamin biosynthesis; Porphyrin biosynthesis; SEQUENCE 443 AA; 50205 MW; EA8D66D0FC9ED212
                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable cobyrinic acid A,C-diamide synthase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 94.5; 20.6%; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67583; AAB99432.1;
TIGR; MJ1421; -.
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                                                                                                                       STANDARD;
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70; Conserv
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-DSPRDAKSII
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                                                                                                                    COBB_METJA
Q58816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oli K-12
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SEQUENCE FROM N.A.
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman I Courtney L., Porwollik S., Ali J., Dante M., Grewal N., Mulvaney E., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heinrichs D.E., Monteiro M.A., Perry M.B., Whitfield C.; "The assembly system for the lipopolysaccharide R2 core-type of Escherichia coli is a hybrid of those found in Escherichia coli K-and Salmonella enterica. Structure and function of the R2 Waak and Waal homologs.";
289 ADI-----LYIGGGYPELFKEELSRNKEMIESIKEFDGYIYGECGGL-MYITKSIDNVPM
                                                                                          VGLLNCSAVMTKHVQGLSYVKAEFLEDCLIGRKGLKFKGHEFHYSKLVNIKEERFAYKIE
                                                         -- ENMDREDIKMLVK
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PATHWAY: LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS.

SIMILARITY: TO E.COLI RFAI AND TO RFAJ.

CAUTION: REF.3 AND REF.4 SEQUENCES DIFFER FROM THAT SHOWN DUE FRAMESHIFTS AND OTHER SEQUENCING ERRORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GROUP
                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eic Acids Res. 18:6128-6128(1990).
FUNCTION: ADDS THE GALACTOSE(I) GROUP ON THE GLUCOSE(I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carstenius P., Flock J.-I., Lindberg A.; "Nucleotide sequence of rfal and rfaJ genes encoding lipopolysaccharide glycosyl transferases from Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                (EC
                                                       VYNL-VLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEE--
                                                                                                                                 KWWDIYND-ESLDYKNVVIGDSHKKQQTLQQFIEALSEAG
                                                                                                                                                                   RGRGIINNLDGIFNGKVLAGYLHNHAVANPYFASSMVNFG
                                                                                                                                                                                                                                                             FFAI_SALTY STANDARD; PRT; 337 AA. P19816; 068267; 01-FEB-1991 (Rel. 17, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Lipopolysaccharide 1,3-galactosyltransferase RFAI OR WAAI OR STM3718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF 198-337 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 273:8849-8859(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-LT2;
MEDLINE-98204873; PubMed-9535865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-91045080; PubMed-2235496;
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Submitted (JUL-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                           Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                 -WTK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eurypelma californica (American tarantula).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
NCBI_TaxID=29932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=84059635; PubMed=6357986;
Schneider H.-J., Drexel R., Feldmaier G., Linzen B., Lottspeich
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MEDLINE=90319102; PubMed=2371273;
Voll W., Voit R.;
"Characterization of the gene encoding the hemocyanin subunit the tarantula Eurypelma californicum.";
Proc. Natl. Acad. Sci. U.S.A. 87:5312-5316(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Henschen A.; "Hemocyanins in Spiders, XVIII. Complete amino-acid sequence subunit e from Eurypelma californicum hemocyanin."; Hoppe-Seyler's Z. Physiol. Chem. 364:1357-1381(1983).
                                                                                                                                                                                                                                                           Length 337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 FKDIYKPIPPVYNLVLAMLWRHPENI--ELDQVKV-VHYCAAGAKPWRFTG
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                                                      EMBL; AF026386; AAC16412.1; -.
EMBL; AE008873; AAL22577.1; -.
EMBL; X53847; CAA37841.1; ALT_FRAME.
PIR; S12097; S12097.
StyGene; SG10337; rfa1.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Lipopolysaccharide biosynthesis; Glycosyltransferase;
                                                                                                                                                                                     -> RE (IN REF. 1).
-> Q (IN REF. 1).
6DB1FA1531AE25F7 CRC64
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                                                                                                                                                                                                                                                    Score 93.5; DB pred. No. 0.88;
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(Rel. 14, Last sequence up
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91060544; PubMed=2246235;
Voit R., Feldmaier-Fuchs G.;
"Arthropod hemocyanins. Molecular encoding the tarantula hemocyanin
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210 E
38905 MW;
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20.3%;
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Best Local Similarity
                                                                                                                                                                                                               337 AA;
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01-APR-1990 (
01-MAR-2002 (
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P02242;
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us-09-810-506-2

E411052A80814004 CRC64;

71545 MW;

623 AA;

SEQUENCE

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OXYGEN CARRIERS
OF MANY MOLLUSKS AND
                                                                                                                                                                                                                                                                                                                                                                                                        H SEVEN
                                                                                                                                                                                    cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITROGEN
HARE A
                                                        MEDLINE=86300721; Pubmed=3017715;

WEDLINE=86300721; Pubmed=3017715;

Voit R., Schneider H.-J.;

"Tarantula hemocyanin mRNA. In vitro translation, cDNA cloning nucleotide sequence corresponding to subunit e.";

Eur. J. Biochem. 159:23-29(1986).

-!- FUNCTION: HEMOCYANINS ARE COPPER-CONTAINING OXYGEN CARRIERS OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSK ARTHROPODS.

-!- SUBUNIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEDIFFERENT CHAINS IDENTIFIED.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: HEMOLYMPH.

-!- TISSUE SPECIFICITY: HEMOLYMPH.

-!- TISSUE SPECIFICITY: HEMOLYMPH.

-!- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROCLIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN ADDITION TO BINDING OXYGEN.

-!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         z
. Chem. 265:19447-19452(1990)
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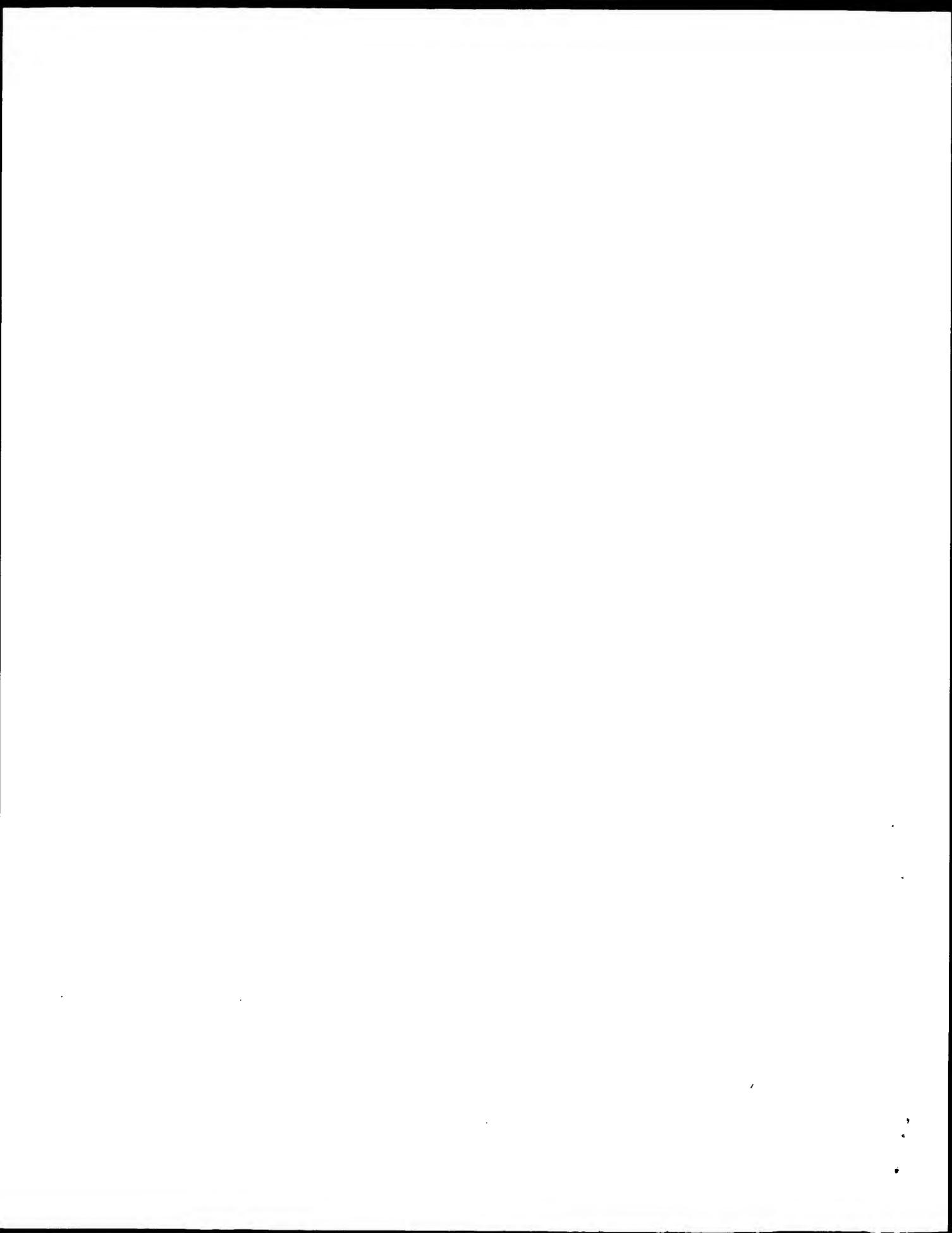
EMBL outstation -strictions on its t is in no way and for commercial b-sib.ch/announce/ a collaboration This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).

HSSP; P04253; 10XY.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR002227; Tyrosinase.
Pfam; PF00372; hemocyanin; 1.
PRINTS; PR00187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN.
PROSITE; PS00498; TYROSINASE.2; 1.
Transport; Oxygen transport; Copper; Ginit. JOINED. JOINED. JOINED. JOINED. JOINED. 4; CAA34772.1; -CAA34643.1; -0; CAA34643.1; -1; CAA34643.1; -2; CAA34643.1; -3; CAA34643.1; -3 EMBL; X16894; EMBL; X04291; EMBL; X16650; EMBL; X16651; EMBL; X16652; EMBL; X16652; EMBL; X16654; EMBL; X16655; EMBL; X16655; EMBL; X16655; EMBL; X16655; EMBL; X16655; EMBL; X16655;

(PROBABLE) Glycoprotein; Hemolymph. 3) COPPER 1 (PROBABLE).
COPPER 1 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
COPPER 2 (PROBABLE).
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (
D -> R (IN REF. 2).
R -> K (IN REF. 2).
A -> H (IN REF. 2).
K -> R (IN REF. 2).
K -> R (IN REF. 2).
H -> M (IN REF. 2).
K -> H (IN REF. 2).
K -> H (IN REF. 2).
C -> D GR (IN REF. 2).
C -> D (IN REF. 2). REF NI) Пq CGW NGH F -> CONFLICT DISULFID CARBOHYD CONFLICT METAL METAL METAL METAL METAL

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11;
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                                                                                                      123 QVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQ-YKIGYCQQCPDKVTWPEAKLGPKPP 181
                       Gaps
                                                                 79
                                                           31;
                                                                                                                                                   Length 623;
                                                                                                                                    241 LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMD -- REDIKMLVKKW-WDI
                       Indels
                     73;
 DB 1;
Score 93.5; DB Pred. No. 1.9; 4; Mismatches
                       24;
5.1%;
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Conservative 2.
            Similarity 45; Conser
 Query Match
Best Local S
Matches 45
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2, 2002, 12:15:10 Search completed: July Job time: 372 sec



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version 4.5 - 2000 Compugen Ltd.
GenCore
Copyright (c) 1993
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- protein search, using sw model OM protein

conds July Run on:

cell updates/sec 2, 2002, 12:14:44; Search time 48.67 Sec (without alignment 1190.740 Million o

US-09-810-506-2 1816 Title: Perfect score:

1 MAPEINTKLTVPVHSATGGE.........FIEALSEAGALQYVKAPSAA 335 Sequence:

0.5 Gapext BLOSUM62 Gapop 10.0 , Scoring table:

562222 seqs, 172994929 residues Searched:

562222 Total number of hits satisfying chosen parameters:

0 2000000000 seq length: seq length: Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

SPTREMBL_19:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_nvertebrate:*
sp_mammal:*
sp_ntc;*
sp_phage:*
sp_phage:*
sp_rodent:*
sp_rodent:*
sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	Q9fxb2 arabidopsis O80518 arabidopsis O22893 arabidopsis Q9xej7 brassica na Q9xgg4 pisum sativ Q40710 oryza sativ O22693 arabidopsis Q9xgn4 ajuga repta Q9xgn3 ajuga repta Q9xgn3 ajuga repta Q9stq9 arabidopsis Q9ffa1 arabidopsis Q947q8 lycopersico Q947q8 lycopersico Q980766 arabidopsis Q947q8 lycopersico
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	DB	
	Length	
	% Query Match	
	Score	1816 1516.5 1390.5 1345.5 1298.5 1219 1216.5 1198.5 1198.5 1198.5 1198.5 1153.5 763.5
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5 Q9W2J6 10 Q940B 10 Q9LSB 10 Q9FZ3 3 O43061	10 094H 2 05323 10 098Z 5 02299 5 09505	16 0918 12 0958 12 0996 12 0996 12 0962	12 09PZ0 16 097P7 10 00403 10 02350 3 09Y761	10 0920P4 12 09E7P3 2 050948 5 2 09REX5 5 3 043062 8 16 097P77 1 2 P96945
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ALIGNMENTS

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		sequence update)	(Tremblrel. 19, Last annotation update) ACTINOL SYNTHASE (AT1G56600/F25P12_16).		Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	a; magnollopnyta; eualcotyledons; core e Brassicales; Brassicaceae; Arabidopsis.			onn L., Ha	Nguyen M., Lam B., Southwick A., Bei, Buehler E., Chin	owng B., F	Liu S., Mu	Thaveri	M., Walker M., Yu G., Ecker J., Theologis A., Davis K.W.;	ppo da caba		eyers M.C.	th A.D., F	Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,	X., Mirand	.K., Quacr Toriumi	., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis			(OCT-2001) to the EMBL/GenBank/DDBJ databases		Kim C.J., Koesema E., Meyers M.C	J.M., Goldsmith A.D.,	
	335 AA.	neuce 1	otatio 600/F2	s).	ta; Eml	tyledom ae; Ara			.B., C	ick A.	A., H	u K.,	nn P.,	T. '.D	Dalle		E., M	oldsmi	iya A.	Liu S	rnam r	Ж., Ŭ			Bank/D		., Koe	е Ј.М.	
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Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,

Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Arabidopsis cDNA clones.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC009323; AAG09103.1; -.

R EMBL; AX058238; AAL15412.1; -.

R EMBL; AX058238; AAL15412.1; -.

R EMBL; AX050410; AAK91426.1; -.

InterPro; IPR002495; Glycosyl_transf_8.

Pfam; PF01501; Glyco_transf_8; 1.

SEQUENCE 335 AA; 38515 MW; O4F52C60B8A3F9D8 CRC64;
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Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.R., Au M., Araujo R., Buehler E., Dewar K., Feng J., Kim C., Li Y., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                     1 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLV
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                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F14J9.1 PROTEIN (WATER STRESS INDUCED PROTEIN-LIKE PROTEIN)
F14J9.1.
                                                                                                                                                                                                                                                          Length
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Pred. No. 1.8e-161;
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nes 335; Conservative
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STRAIN=CV. COLUMBIA;
MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                              180
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE.
AT2G47180 OR T8113.2/AT2G47180.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                           Length 334;
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      Shinozaki
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0D09CA497B392BA2 CRC64
    Yamada K.,
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Pred. No. 1.8e-133;
); Mismatches 24;
Sakurai T., Satou M., Seki M., Shinn P., Yamad Ecker J., Theologis A., Davis R.W.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AC003970; AAC33195.1; -.
EMBL; AF370546; AAK48973.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 334 AA; 38677 MW; 0D09CA497B392BP
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80.9%;
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                                                                                                                                                                                                                                                                                          Gaps
SEQUENCE FROM N.A.

Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee C.,

Youndera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,

Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.

Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,

Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Shinn P.,

Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
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|WKFVEY
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                               "Full Length cDNA of gene T8113.2/At2g47180 (GI:2275196)."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002337; AAB63818.1; -.
EMBL; AY056139; AAL07218.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 344 AA; 39596 MW; 46784EA16DBD3A46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRI
                                                                                                                                                                                                                                                                                                                                                                                       -NTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLR
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF106954; AAD26116.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                               DB 10;
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                                                                                                                                                                                                                                                  Score 1390.5; DB 10;
Pred. No. 1.1e-121;
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74.78;
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01-NOV-1999
01-JUN-2001
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE (EC 2.4.1.123).
Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidaeeurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
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                                                                                                                             TKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDH
                                                                                132 NIDHLFDLPDGYFYAVMDCFCEKTWSHTPQYKIGYCQQCPEKVQWPKEELGEPPSLYFNA
                                                                                                                                                                                                                                                                                                                               247 NIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDS
                                                                                                                                                                                                                                                                                                                                                 MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP
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                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=EMBRYO (AXIS AND COTYLEDONS);
Jones R.G., Harrison C.J., Hedley C.L.;
Cloning of Galactinol synthase from Pea embryo.";
L.Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ243815; CAB51130.1; -.
R. InterPro; IPR002495; Glycosyl_transf_8.
R. InterPro; IPR002495; Glycosyl_transferase.
R. Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycosyltransferase.
Transferase; Glycosyltransferase.
 Length
                                Indels
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; DB 10;
1.9e-121;
nes 35;
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                  ed. No. 1.90
Mismatches
Score 1388;
Pred. No. 1
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TISSUE=EMBRYO (AXIS AND COTYLEDONS);
                             35;
  76.48;
76.48;
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nes 245; Conser
                  1 Similarity
253; Conser
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   Query Match
                    Best Local
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LDYKK
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                                    PLYFNAGMFVY EPNLSTYHNLLETVK IVPPTLFAEQDFLNMY FKDIYKPIPPVYNLVLAM
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                                                                                genes in
                                                                                                                                                                              040710;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
WSI76 PROTEIN INDUCED BY WATER STRESS.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=SOMEWAKE;
MEDLINE=95036005; PubMed=7948880;
Takahashi R., Joshee N., Kitagawa Y.;
Tinduction of chilling resistance by water stress, and analysis and expression of water stress-regulated generally D26537; BAA05538.1; ...
InterPro; IPR002495; Glycosyl_transf_8.
Frant PF01501; Glyco_transf_8; 1.
SEQUENCE 328 AA; 37698 MW; D87DECDAA7AF98B7 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                   Score 1319; DB 10;
Pred. No. 5.2e-115;
41; Mismatches 48;
                                                                                                            335
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                                                                                                           VVIGDSHKKQQTLQQ-FIEALSEAGALQYVKAPSAA
                                                                                                                     VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
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                                                                                                                                                                                                                                                                                                                                                                                                   Match 72.6%;
Local Similarity 71.0%;
les 238; Conservative
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Matches
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                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                         Kim C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334;
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                                                                                                                                                                                                                                                              Federspiel N.A., Palm C.J., Conway A.B., Kurtz D.B., Conway A.B., Araujo R., Brendel V., Buehler E., Dewar K., Feng J., Li Y., Oji O., Osborne B.I., Shinn P., Sun H., Toriumi M., Vysotskaia V.S., Yu G., Ecker J., Theologis A., Davis R.W.; "Genomic sequence of Arabidopsis."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AC002292; AAB71970.1; -.
InterPro; IPR002495; Glycosyl_transf_8.

InterPro; IPR002495; Glycosyl_transf_8.

SEQUENCE 334 AA; 38511 MW; 591D3D441F01FA75 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
Asteridae; euasterids I; Lamiales; Lamiaceae; Ajuga.

NCBI_TaxID=38596;
                                    Created)
Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GALACTINOL SYNTHASE, ISOFORM GOLS-1 (EC 2.4.1.123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1298.5; DB 10;
Pred. No. 4.4e-113;
5; Mismatches 52;
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299 FKSKIPADAEETVTKSSILASVLEP--
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larity 70.7%;
Conservative 35
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241; Conser
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01-JAN-1998 (TrE
01-DEC-2001 (TrE
F8A5.2 PROTEIN.
F8A5.2.
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Matches 241
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Q9XGN4;
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dicots; Rosidae;
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                                                      galactinol
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Theologis
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                    roles of two distinct
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submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF412094; AAL06547.1; -.
SEQUENCE 221 AA; 25759 MW; 30D65575CB2D706C CRC64;
                                                                                                                                                  B3D575F9084DFF6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annotation update)
                                                                                                                                                                                          DB 10;
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                                        oligosaccharides
the roles of two
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Pred. No. 8.8e-112;
88; Mismatches 41;
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                                                           synthases.";

Plant J. 21:249-258(2000).

EMBL; AJ237693; CAB51533.1; ~.

InterPro; IPR002495; Glycosyl_transf_8.

Pfam; PF01501; Glyco_transf_8; 1.

Transferase; Glycosyltransferase.

Transferase; Glycosyltransferase.

erouence 333 AA; 37881 MW; B3D575F9
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              PubMed=10758476;
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                                         family
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SEQUENCE FROM N.A.
MEDLINE=20224020; PubMed=107584
Sprenger N., Keller F.;
"Allocation of raffinose family
storage pools in Ajuga reptans:
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Local Similarity 73.0%;
Les 233; Conservative
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the roles of two distinct galactinol
           Gaps
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                                                                                                                                  NLVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots,
Asteridae; euasterids I; Lamiales; Lamiaceae; Ajuga.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GALACTINOL SYNTHASE, ISOFORM GOLS-2 (EC 2.4.1.123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.0%; Score 1216.5; DB 10;
llarity 75.4%; Pred. No. 1.7e-105;
Conservative 29; Mismatches 39;
                                                                                                                                                                                   335
Pred. No. 6.7e-106;
Mismatches 0;
           ő
                                                                                                                                                                                   SLDYKNVVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                                                                                               synthases.";
Plant J. 21:249-258(2000).
EMBL; AJ237694; CAB51534.1; -.
InterPro; IPR002495; Glycosyl_transf_8
Pfam; PF01501; Glyco_transf_8; 1.
Transferase; Glycosyltransferase.
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larity 100.0%;
Conservative
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Best Local Similarity
Matches 224; Conser
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Local Similarity
nes 221; Conser
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01-NOV-1999
01-DEC-2001
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01-DEC-2001
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dicots; Rosidae
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                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                 Lemcke K.,
databases.
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                                                                                                                                                                                   Bevan M., Koetter P., Hempel S., Entian K.-D., Bancroft
Mewes H.W., Mayer K.F.X., Schueller C.;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       EU Arabidopsis sequencing project;
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                                                                                                                                                                F10846E37ACF95F1 CRC64;
                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                             66.0%; Score 1198.5; DB 10;
larity 65.0%; Pred. No. 1.1e-103;
Conservative 31; Mismatches 61;
                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL049171; CAB38954.1; -.
EMBL; AL161564; CAB79480.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
Hypothetical protein.
SEQUENCE 361 AA; 41906 MW; F10846E37ACF95F
                                                                                                                                                                                                                                                                   EQUENCE FROM N.A. ose M., Hempel S., Entian K.-D., Mewes H.W., ubmitted (MAR-2000) to the EMBL/GenBank/DDBJ
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                                                                                       HYPOTHETICAL 41.9 KDA PROTEIN T25K17.60 OR AT4G26250.
                                       PRELIMINARY;
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Best Local
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Sequence
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edons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                    MEDLINE=97471969; PubMed=9330910;
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequena
features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidentosids II; Brassicales; Brassicaceae; Arabidopsis.
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EE8BEFB82FBBEAA3 CRC64;
                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Last annotation update)
                         update)
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..1e-103;
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 Created)
Last sequence up
Last annotation
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Mismatches
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EMBL; AB005244; BAB10052.1; -.

InterPro; IPR002495; Glycosyl_transf_8.

Pfam; PF01501; Glyco_transf_8; 1.

SEQUENCE 333 AA; 38472 MW; EE8BEFB
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(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 66.0%;
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08,
19,
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                                                            GALACTINOL SYNTHASE.
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STRAIN-CV. COLUMBIA,
Vysotskaia V.S., Scl
                                                                                                                                                                                                                SEQUENCE FROM N.A.
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MEDLINE-97471969;
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  A.B.
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eudicots;
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   E.,
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N.A.
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                                                          "Arabidopsis thaliana chromosome 1 BAC T13D8 sequence." Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
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Spermatophyta; Magnoliophyta; eudicotyledons; core el
Asteridae; euasterids I; Solanales; Solanaceae; Solan
NCBI_TaxID=4081;
Liu S., Li J., Araujo R., Au M., Brendel V., Buehler Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE GALACTINOL SYNTHASE 1 (EC 2.4.1.123).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         335
                                                                                                                                                                                                                                                   61.1%; Score 1110; DB 10;
larity 59.9%; Pred. No. 1.9e-95;
Conservative 46; Mismatches 64;
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Downie B., Dahal P., Nonogaki H., Gurusinghe S Alvarado V., Bradford K.J.;
"Galactinol synthase gene expression in tomatc Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AF311943; AAL26804.1; -.
Transferase; Glycosyltransferase.
SEQUENCE 318 AA; 36402 MW; AE66D71E45097E5
                                                                                                                                               Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
EMBL; AC004473; AAC24075.1; -.
InterPro; IPR002495; Glycosyl_transf_8.
Pfam; PF01501; Glyco_transf_8; 1.
SEQUENCE 345 AA; 39372 MW; B4EDDE0FDA075E6
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                                                                                                                     COLUMBIA;
                                                                                                                                                                                                                                                                   Local Similarity
Les 203; Conser
                                                                                                        SEQUENCE FROM N.A
                                                                                                                    STRAIN=CV. CO
Theologis A.;
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01-DEC-2001
01-DEC-2001
01-DEC-2001
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Best Local
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1; Tracheophyta;
eudicots; Vitaceae;
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 Gaps
                                               56
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                                                                       PKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLV
                                                                                                                                                                                                                     LAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLD
                                                                                                                                                                                                                               LAMLWRHPEKIEVNKAKAVHYCSPGAKPWKYTGKEEHMDREDIKMLVKKWWDIYNDTTLD
                                                                                                                      LDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG
                                                                                                                                              ---YGEPCDEVLPWPK-ELG
                                                                                                                                                                                  213;
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39;
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"Freezing tolerance in grape flower buds.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases

EMBL; AF178569; AAD55726.1; -.

InterPro; IPR002495; Glycosyl_transf_8.

Pfam; PF01501; Glyco_transf_8; 1.

NON_TER 1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core evitis.
                                                                                                                                                                                                                                                                                  --HKAQGST---VEANRLRGAAFSDTNISALYITSPSAA
                                                                                                                                                                                                                                                                      -LQYVKAPSAA
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
GALACTINOL SYNTHASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 763.5; DB 10;
Pred. No. 2.4e-63;
2; Mismatches 15;
57;
                                                                                                                                    117 LDGDMQVFENIDHLFELPDKYLYAVADCICDM----
  Mismatches
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48;
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ilarity 80.9%;
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5

2002, 12:14:44

2,

completed: July

Search

318;

Length

DB 10;

Score 1053.5; DB Pred. No. 3.3e-90;

58.0%; 58.4%;

Best Local Similarity

Query Match

Job time: 376 sec

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4.5
Compugen Ltd
GenCore version Copyright (c) 1993 - 2000
```

- protein search, using sw model OM protein

2, 2002, 12:09:33 ; Search time 29.88 Seconds (without alignments) 1077.307 Million cell updates/sec July Run on:

US-09-810-506-2 1816 1 MAPEINTKLTVPVHSATGGE...

.....FIEALSEAGALQYVKAPSAA 335 Title: Perfect score: Sequence:

Gapext BLOSUM62 Gapop 10.0 , Scoring table:

283138 seqs, 96089334 residues Searched:

0.5

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1264 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable galactino	ypothetical pr	robable qalactin	SI76 protein -	potheti	thetical pr	pothetical p	hetical pr	0	qlucos	aj	ŭ	hc hc	al	ical pr	cal	ical pr	transf	protein F7G19.14 [cal prot	cical pro	glycc	cal prot	syl trans	qlycosyl transfera	ein -	protei	eneral stress	bable membra
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301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335

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517 696	814	335	335	394	1251	2157	~	_	311	337	338	624	4589	
6.0	•	•	•	•	•	•	•	•	•	•	•	•	•	5.5
108.5	108	107	107	106	105	103.5	101	97.5	97.5	96.5	96.5	96.5	95	94.5
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ULT 1 bable galactinol synthase F2; bable galactinol synthase F2; becies: Arabidopsis thaliana ate: 02-Mar-2001 #sequence_rcession: G96607 beologis, A.; Ecker, J.R.; Pain, C.W.; Chung, M.K.; Conn, en, N.F.; Hughes, B.; Huizar, ure 408, 816-820, 2000 uthors: Hunter, J.L.; Jenkins i. Li, J.H.; Li, Y.; Lin, X.; zo, M.; Rooney, T.; Rowley, i to, M.; Wu, D.; Yu, G.; Fraser, itle: Sequence and analysis of terence number: A86141; MUII ccession: G96607 tatus: preliminary olecule type: DNA esidues: 1-335 <sto> tatus: preliminary olecule type: GB:AE005173; ene: F25p12.95 ap position: 1 MAPEINTKLTVPVHSATGGEKE </sto>		SP12.95 [imported] - Arabidopsis thaliana (mouse-ear cress) evision 02-Mar-2001 #text_change 31-Mar-2001 alm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, L.; Conway, A.R.; Conway, A.R.; Creasy, T.H.; Dewar, L.; Conway, A.R.; Conway, A.R.; Creasy, T.H.; Dewar, L.; Conway, A.R.; Con	Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia D.; Sakano, H. artz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo, C.M.; Venter, J.C.; Davis, R.W. of chromosome 1 of the plant Arabidopsis. D:21016719 : NID:g9954752; PIDN:AAG09103.1; GSPDB:GN00141	tch al Similarity 100.0%; Score 1816; DB 2; Length 335; 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0; MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60		PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM 240
ULT 1 bable g pecies: ccessic ccessic nure 408 uthors: i, Li, X whith with a sidues ccessic ctatus: litle: S eferenc ccessic to Li, X whith with a sidues ccessic ctatus: litle: S eferenc ccessic litle: S eferenc ccessic litle: S ap posi litle: S ctatus: litle: S ap posi litle: S ctatus: litle: S ctatus: litle: S litle: S litle: S concined litle: S litle:	RESULT G96607 C96607 C; Species: C; Accessic A; Authors: Ker, M.; Wartile: C; Genetics A; Authors: A;	alactinol synthase F25 Arabidopsis thalianaMar-2001 #sequence_re n: G96607 S, A.; Ecker, J.R.; Pa 1.; Chung, M.K.; Conn, 1.; Hughes, B.; Huizar, 1.; 816-820, 2000 Hunter, J.L.; Jenkins	J.H.; Ll, Y.; Lln, X.; Rooney, T.; Rowley, D. Salzberg, S.L.; Schwar Al, D.; Yu, G.; Fraser, equence and analysis of e number: A86141; MUID: n: G96607 preliminary type: DNA : 1-335 <sto> : 1-335 <sto> : 1-335 <sto> : type: DNA : 1-35 <sto> : type: DNA : 1-305 <sto> : thon: 1</sto></sto></sto></sto></sto>	tch 100.0% 335; Conservative MAPEINTKLTVPVHSATGGEKR MAPEINTKLTVPVHSATGGEKR MAPEINTKLTVPVHSATGGEKR DVPEDHRKQLVDQGCVVKEIEP	DVPEDHRKQLVDQGCVVKEIEP DIQVEDNIDHLFDLPNGQFYAVI	PLYFNAGMFVYEPNLSTYHNLLI
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GSPDB:GN00139

2

Gaps

6

Indels

Length

2

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172

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C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-200(C; Accession: T07610
R; Takahashi, R.; Joshee, N.; Kitagawa, Y.
R; Takahashi, R.; Joshee, N.; Kitagawa, Y.
Plant Mol. Biol. 26, 339-352, 1994
A; Title: Induction of chilling resistance by water stress, and cDNA sequence, T10410
A; Reference number: S52642; MUID: 95036005
A; Ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYN
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                    A; Residues: 1-344 <STO>
A; Cross-references: GB:AE002093; NID:g2275196; PIDN:AAB63818.1; C; Genetics:
A; Gene: At2g47180
A; Map position: 2
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Pred. No. 9.3e-108;
L; Mismatches 47;
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larity 74.7%;
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Marziali,
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Maiti, R
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-]
C; Accession: A84912
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Uleuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Friente 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidop A; Reference number: A84420; MUID: 20083487
A; Accession: A84912
A; Status: preliminary
                                                                                                                                 hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.5%; Score 1516.5; DB 2, 80.9%; Pred. No. 3.1e-118; tive 30; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVI-----GDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
  301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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sequence analysis

#text_change 21-Jul-2000

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                          Gaps
                                               MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP
                                                                                                                                               DVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDG
                                                                                                             8
Length 328;
                         Indels
72.6%; Score 1319; DB 2; 71.0%; Pred. No. 7.5e-102; ative 41; Mismatches 48;
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Oji, O.; Liu, S.;
c, J.R.; Federspiel
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                        Mayer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T13D8.32 - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear cress)

C; Species: Arabidopsis thaliana (Mouse-ear cress)

C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 22-Oct-1999

C; Accession: T02295

R; Vysotskaia, V.S.; Schwartz, J.R.; Kwan, A.; Toriumi, M.; Yu, G.; Oji, O.; Liu, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Fedensubmitted to the EMBL Data Library, June 1998

A; Description: Arabidopsis thaliana chromosome 1 BAC T13D8 sequence.

A; Reference number: 214649

A; Accession: T02295

A; Accession: T02295

A; Accession: T02295

A; Concle type: DNA

A; Residues: 1-345 < VYS>
A; Cross-references: EMBL:AC004473; NID:g3108025; PID:g3249091; GSPDB:GN00059; A; A; Genetics:

A; Map position: 1

A; Map position: 1

A; Map position: 1

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A; Map position: 1
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                     H.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175
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                                                                                                                                                                                                                                                                                                                                                                                                                LGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYN
                                                                                                                                                                                                                                                                                                                              KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVLAMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDES
                       Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                            361;
C; Accession: T06009
R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Me submitted to the Protein Sequence Database, March 1999
A; Reference number: 215382
A; Accession: T06009
A; Molecule type: DNA
A; Residues: 1-361 <BEV>
A; Residues: 1-361 <BEV>
A; Cross-references: EMBL: AL049171; GSPDB: GN00062; ATSP: T25K17.60
A; Experimental source: cultivar Columbia; BAC clone T25K17
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Hatrons: 136/3; 244/3; 289/3
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                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                           61;
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Pred. No. 1.8e-84;
                                                                                                                                                                                                                                                         Score 1198.5; DB
Pred. No. 8.6e-92,
; Mismatches 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                                                         66.0%;
illarity 65.0%;
Conservative 3.
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59.9%;
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ses 221; Conser
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Best Local S
Matches 221
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Best Local S
Matches 203
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                                                                                                                                                                                                                                                                                                                              Q
                                                                                                                                                                                                                                                                                                        O.; Alonso, Dowar, K.;
                                                                                                                                                                                                                                                                                                                                                                              S.; Khaykin, E.; Kim, C.S.; Maiti, R.; Marziali
                                                                                                                                                                                                                                                                                                                                                                                                                                Tallon,
                                                                                                                                                                                                                                                                                                                                                                                                                                Н.;
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                                                                                                                                                                                                                                                                                                          Creasy, T.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
T06009
hypothetical protein T25K17.60 - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                A.M.; Sun,
                                                                                                                                                                                                                                                                           31-Mar-2001
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|YSKMIY
                                                  1 MAPEINTK --- LTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVA
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H96629
hypothetical protein F8A5.2 [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Hext_change 31-M
C;Accession: H96629
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Crea ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidop A;Reference number: A86141; MUID:21016719
A;Accession: H96629
A;Status: preliminary
A;Accession: H96629
A;Cross-references: GB:AE005173; NID:g2462751; PIDN:AAB71970.1; GSPD C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34;
178 PLYFNAGMFVHEPGLGTAKDLLDALVVTPPTPFAEQDFLNMFFREQYKPIPNVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.5%; Score 1298.5; DB 2 70.7%; Pred. No. 3.9e-100; tive 35; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- EMTYFPAPSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YKNVVIGDSHK - - - KQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                      335
                                                                                                                                                       328
                                                                                                                     301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                                       ----EEDNADEASQPMRTALAEAGAVKYFPAPSAA
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Qy 80 IEPVYPPENQTEFAMAYYVINYSKLRIW	lucosyltransferase (EC 2.4.1.186) - hu names: glycogenin
Qy 119 DGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGP 178 	giycogen(starcn) synthase, giycogenin subunit omo sapiens (man) ay-1999 #sequence_revision 21-May-1999 #text_change 11-Jun-1999 JC4695; G01948; S45141
Qy 179 KPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVL 238 	F.; KOCCHI, M.; BOSSOIASCO, M.; COIGEIA, K.; SDIACCIA, F., FINELLI, F., phys. Res. Commun. 220, 72-77, 1996 human skeletal muscle glycogenin gene: cDNA, tissue expression, and chr number: JC4695; MUID:96176958
OY 239 AMLWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDY 298 :: ::	JC4093 Ype: mRNA 1-333 <bar> rences: GB:U441</bar>
Qy 299 KNVVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335 : : :	I.R. the EMBL Data Library,
protein T14N5.1 - Arabidopsis thaliana abidopsis thaliana (mouse-ear cress)	ced from GB/EMBL/DDBJ NRNA <rod> S: EMBL:U31525; NID:g976399 Smann, S.; Ansorge, W.</rod>
<pre>01-Feb-1999 #sequence_revision 01-Feb-19 ion: T00444 ipiel, N.A.; Palm, C.J.; Conway, A.B.; Ku kaia, V.S.; Yu, G.; Ecker, J.; Theologis id to the FWRL Data Library, September 19</pre>	the EMBL Data n: Cloning and number: S45140 S45141 vpe: mRNA
ion: T00444 translated from GB/EMBL/DDBJ	A;Residues: 1-203,'KMSQEPYHICPLGRSQLWHSRLYPRKNGR','NDGNRARLIIWEQIPLTTSRGNLTLTSSR','NT A;Cross-references: EMBL:X79537; NID:g496894; PIDN:CAA56073.1; PID:g496895 C;Genetics:
les: 1-1201 <fed> references: EMBL: ACO</fed>	GYG rences: GDB:1326953 on: 3q24-3q25.1
ATSP:T14N5.1 Sition: 1 ns: 251/1; 569/1; 601/2; 858/1	n: c nin lyco ired
Query Match Best Local Similarity 24.2%; Score 258.5; DB 2; Length 1201; Matches 85; Conservative 50; Mismatches 117; Indels 99; Gaps 12;	erraminy: y vords: acet odified sit Binding si
Qy 4 EINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAK 49 :: :	Query Match Best Local Similarity 24.8%; Pred. No. 2.4e-12; Matches 78; Conservative 43; Mismatches 120; Indels 74; Gaps 11;
Qy 50 SKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEF 109 	QY 22 RAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKE 79
Qy 110 VEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKV 169 : : : : : Db 953 TEYSKIIFIDADMLILRNIDFLFE	QY 80 IEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139 : : : :
QY 170 TWPEAKLGPKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKP 229 :	Qy 140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199
Qy 230 IPPVYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPW 266 	Qy 200 NLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQ 252
Qy 267RFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDSHKKQ 310 : : : : Db 1092 VDIFGEFASDEAHKTWWRVHDAMPENL-HKFCLLRSKQKAQ 1131	253 VKVVHYCAAGAKPWRFT- : : 208 AKVVHFLGR-VKPWNYTY
•	Qy 302 VIGDSHKKQQTLQQF 316

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hypothetical protein T24C10.6 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: H96590
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
R; Zzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: H96590
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C; Species: Schizosaccharomyces pombe
C; Species: Schizosaccharomyces pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C; Accession: T40489
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, submitted to the EMBL Data Library, February 1998
A; Reference number: Z21910
A; Reference number: T40489
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263 FGLVQDTCSYQHVEDVSGAVSHLSLGETPATTQPFVSSEERKERWEQGQADYMGADS
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-557 <STC
A; Cross-references: GF
C; Genetics:
A; Gene: T24C10.6
A; Map position: 1
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A; Modecule type: protein
A; Residues: 1-87, 'S', 89-96, 'L', 98-332 <CAM>
R; Pitcher, J.; Smythe, C.; Campbell, D.G.; Cohen, P.
Eur. J. Biochem. 169, 497-502, 1987
A; Title: Identification of the 38-kDa subunit of rabbit skeletal muscle gl:
A; Reference number: $02470; MUID:88082782
A; Reference number: $02470; MUID:88082782
A; Residues: 9-19; 38-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
C; Function:
A; Residues: 9-19; 38-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
C; Function:
A; Residues: 9-19; 38-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
C; Function:
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C; Function:
A; Residues: 9-19; 38-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
C; Function:
A; Residues: 9-19; 38-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
C; Function:
A; Residues: 9-19; 80-44, 'M'; 90-94; 204-207, 'F', 209-210, 'KH', 213-219 <PIT>
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A; Residues: 9-19; 80-44, 'M'; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-94; 90-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:L01791; NID:g165512; PIDN:AAA31404.1; PID A;Experimental source: skeletal muscle A;Note: sequence is inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIP:120846) R;Campbell, D.G.; Cohen. P
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                                                                                                                                                                                                                                                        #text_change
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                                                                                                                                                        glycogenin glucosyltransferase (EC 2.4.1.186) - rabbit N; Alternate names: glycogen synthase 38K chain; glycogenin C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 21-May-1999 #sequence_revision 21-May-1999 #text_chang C; Accession: A45094; S06482; S02470 R; Viskupic, E.; Cao, Y.; Zhang, W.; Cheng, C.; DePaoli-Roach, J. Biol. Chem. 267, 25759-25763, 1992 A; Title: Rabbit skeletal muscle glycogenin. Molecular cloning A; Reference number: A45094; MUID:93100288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Campbell, D.G.; Cohen, P.
Eur. J. Biochem. 185, 119-125, 1989
A;Title: The amino acid sequence of rabbit skeletal muscle
A;Reference number: S06482; MUID:90032666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 235.5; DB 1;
Pred. No. 6.9e-12;
9; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -DESLDYKNV--VIGD-SH----KKQQTLQQFIEALS---
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Similarity 23.8%;
85; Conservative 49
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                        264
                         PLLOOF
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A: Residues: 1-332 <VIS>
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A45094
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Best Local S
Matches 85
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244 HPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKW
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Pred. No. 2.4e-09;
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A; Accession: T31001
A; Accession: T31001
A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
A; Residues: 1-429 <STE>
A; Cross-references: EMBL:U64599; PIDN:AAB04562.1
A; Experimental source: strain Bristol N2
C; Genetics:
A; Map position: X
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              GMFVYEPNLSTYHNLLETVKIVPPTLF
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Best Local
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                                               SPDB:SPBC4C3.08
                                                                                                                                                                                                  18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AAPNVYESLSDFHRMNS 144
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                                                                                                                                                                                                                                     --YVKGVVGLAKGL 45
                                                                                                                                                                                                                                                                                                                                                                         -PNGQFYAV-MD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PPPFKDYFNAGLFVFKPLK
                                                                                                                                                                                                                                                                      SPEIQRS----VYTLTGLAPSSKMAFVTMLTVRAANGENEVENTQQDWYYNSTRLLVHRL
                                                                                                                                                                                                                                                                                                       46 RK---AKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEPVYPPE-----NQTEFAMAYY
                                                                                                                                                                                                                                                                                                                                                                                            SMMFTKLRVFEMYEYDRICFLDSDILPIKKMDKVFDVHQLSYSKDSVLFPPTLFYKPRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- AYNSAGAFPWESLDWTFN
                                                                                                                                                                                                  91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
A45729
glycogenin homolog, sqdB 3'-region - Rhodobacter sphaeroides
C; Species: Rhodobacter sphaeroides
C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 08-0.
C; Accession: A45729; S27663
R; Benning, C.; Somerville, C.R.
J. Bacteriol. 174, 6479-6487, 1992
A; Title: Identification of an operon involved in sulfolipid biosynt.
A; Reference number: A45729; MUID:93015699
A; Reference number: A45729
A; Cocssion: A45729
A; Residues: 1-260 < BEN>
A; Residues: 1-260 < BEN>
A; Residues: GMBL:M89780; NID:g152038; PIDN:AAA73224.1; PID:C; Genetics:
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---PENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYND 293
                                                                                                                                                                    372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYHNLLETVKIVPPTLF - - - - AEQDFLNMYFKDIYKPIPPVYNLVLAMLWRH - -
                                               GSPDB:GN00067
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                                                                                                                                                                   Length
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                                                                                                                                                                 DB 2;
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Pred. No. 1.6e-09;
6; Mismatches 93;
                                                                                                                                                                                                    128;
                                                                                                                                                                 Score 225.5; DB 2 Pred. No. 5.4e-11;
             A; Molecule type: DNA_A; Residues: 1-372 <WOO>A; Residues: 1-372 <WOO>A; Cross-references: EMBL:AL021730; PIDN:CAA16830.1; A; Experimental source: strain 972h-; cosmid c4C3 C; Genetics: A; Gene: SPDB:SPBC4C3.08 A; Map position: 2
preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                     2 APEINTKLTVPVHSATG---GEKRAYVTFL---AGTGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 IFWRRFTEEFAAYGLTRDDLYPYVFAAVSDPGMWHET --
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                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AHYKRLMALARF -- PKLYDNANMMEQSLLNF ---
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23.2%;
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illarity 25.3%;
Conservative 4
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89; Conser
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Best Local S
Matches 89
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H.W.; Mayer,
                                                                                                                                                                                                                                                                                                                                                             pothetical protein F17M5.90 - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T31001
hypothetical protein F56B6.4 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 29-Oct-1999
C; Accession: T31001
R; Stellyes, L.; Stellye, L.
submitted to the EMBL Data Library, September 1999
submitted to the sequence of C. elegans cosmid F56B6.
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                                                          GVFTARPSTDTYARMLEALDV - - PGAFWRRTDQSFLQQFFPD - WQGLPVFCNMLQYVWFA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 EKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKE 79
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---AEQDFLNMYFKDIYKPIPPVYNLVLAMLWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.; Mewes,
                                                                                                                                                                                                                                                                                                                                                                                                                             C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-C; Accession: T05984
R; Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewe submitted to the Protein Sequence Database, March 1999
A; Reference number: Z15263
A; Reference number: Z15263
A; Accession: T05984
A; Molecule type: DNA
A; Residues: 1-333 < BEV>
A; Residues: 1-333 < BEV>
A; Experimental source: cultivar Columbia; BAC clone F17M5
A; Experimental source: cultivar Columbia; BAC clone F17M5
A; Gene: ATSP:F17M5.90
A; Map position: 4
A; Introns: 193/2
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                                                                                                                                                                         NLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLW----
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A;Introns: 41/3; 105/3; 146/1; 202/2; 245/3; 371/3; 390/3 A;Note: F56B6.4

16; 83 VYPPENQTEFAMAY --- YVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQF 139 --FQQWQKIYHA 240 140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH 199 200 NLLETVKIVPPTLFA------EQDFLNMYF---KDIYKP--IPPVYNLVLAMLW--- 242 ----RHPENIELDQVKVVHYCAAGAKPWR----FTGEEENMDREDIKMLVKKWWDIY-- 291 96; Gaps 23 AYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEIEP 82 Length 429; Indels 10.8%; Score 197; DB 2; I Llarity 23.6%; Pred. No. 1.5e-08; Conservative 46; Mismatches 101; 241 HVNHTSRTNEHAAVFPSH 258 --NDESLDYKNVVIGDSH 307 Query Match Best Local Similarity Matches 75; Conserva 120 SAASD----147 QLVD---292 243 qq a q Q δy Qγ qq g δ Óγ ö

Search completed: July 2, 2002, 12:09:34 Job time: 181 sec /

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Search time 23.19 Seconds (without alignments) 352.849 Million cell updates/sec
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1 MAPEINTKLTVPVHSATGGE...
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length: 2000000000

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Sequence:
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Maximum
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Issued_Patents_AA: Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	dnence	equence 2, A	equence 3,	_ ,	equence 14, Ap	4	20	16	12	4,	4	4	4	4	4	7	20	'n	ω,	3,	7	7	7	10	36, App	Sequence 36, Appl	11
SUMMARIES	di 	S-09-073-297-	-09-073-29	-09-073-297-	-073-297-	-09-073-297-	-09-073-297-	-073-297-2	-073-297-1	-09-073-297-	-312-387B-	-08-683-42	-08-683-45	-08-878-36	-08-478-14	9-333-412-	US-09-073-297-24	-08-961-083-	S-08-753-233-	-984-246-	-09-149-674-	-753-233-	-984-246-	-09-149-674-	-073-297-1	-08-557-122A	8-99	PCT-US93-07923-11
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Gaps

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Indels

Query Match
72.6%; Score 1319; DB 4;
Best Local Similarity 71.0%; Pred. No. 1.2e-138;
Matches 238; Conservative 41; Mismatches 48;

Length 328;

MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60

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Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 1, Appli Sequence 28, Appli		
28 87 4.8 759 5 PCT-US93-07923-2 29 87 4.8 766 1 US-08-230-491A-3 30 87 4.8 766 1 US-08-619-280A-3 31 87 4.8 766 2 US-08-940-391-3 32 87 4.8 766 4 US-09-794-236-1 33 85 4.7 903 1 US-08-750-532-1 34 85 4.7 1398 1 US-08-750-532-9 35 85 4.7 1398 4 US-08-894-818B-8 36 85 4.7 1398 4 US-09-36-952-4 38 82.5 4.5 1398 4 US-09-36-952-4 38 82.5 4.5 775 1 US-08-738-168B-5 40 82.5 4.5 775 1 US-07-966-278-1 41 82.5 4.5 775 2 US-08-556-355A-1 43 82.5 4.5 775 2 US-08-556-355A-1 44 82.5 4.5 775 2 US-08-556-355A-1 45 82.5 4.5 775 2 US-08-557-122A-28	RESULT 1 US-09-073-297-6 Sequence 6, Application US/09073297 Patent No. 6255114 GENERAL INFORMATION: TITLE OF INVENTION: TITLE OF INVENTION: CORRESPONDENCE ADDRESS: ADDRESSE: E. I. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A. ZIP: 19898 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 INCH COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: MICROSOFT WINDOWS 95 SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/073,297 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/852615	FILING DATE: MAY 7, ATTORNEY/AGENT INFORMAT NAME: MAJARIAN, WILL REGISTRATION NUMBER: REFERENCE/DOCKET NUMB TELECOMMUNICATION INFOR TELEPHONE: 302-992-4 TELEFAX: 302-773-016 INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC LENGTH: 328 amino acid STRANDEDNESS: not re TOPOLOGY: linear MOLECULE TYPE: peptide S-09-073-297-6

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EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFY
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                               APPLICANT: LIGHTNE TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: STRANDEDNESS: no
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US-09-073-297-3
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Best Local S
Matches 78
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                                                                                  LAM
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                                  DIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 265.5; DB 4;
Pred. No. 3.6e-21;
                                                                                                                                                                                                                                                                                                                                                         STARCH BIOSYNTHETIC ENZYMES 26
                                                                                                                                                                                                                      301 VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA 335
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                                                                                                                                                                                                                                                                                                                                                JONATHAN EDWARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IS DISKETTE, 3.50 INCH IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         2, Application US/09073297
5. 6255114
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| Larity 27.6%;
| Conservative |
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STANUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                                                                                                                                              LIGHTNER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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81; Conserv
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                                                                                                                                                                                                                                                                                                                      Patent No. 6255114
GENERAL INFORMATION:
APPLICANT: LIGHTN
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MGPNVSSE--
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Best Local 9
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Matches
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                                                          AVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHN
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Length 333;
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    DU PONT DE NEMOURS AND COMPANY

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Pred. No. 1.9e-18;
3; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                              LIGHTNER, JONATHAN EDWARD
FENTION: STARCH BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                  -VVHYCAAGAKPWR-FTGEEENMDREDIKMLVK-
                                                                                                 -ATGNNATL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB-1083-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09073297
Patent No. 6255114
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: E. I. DU PONT DI
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not relevant
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llarity 24.8%;
Conservative 4:
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REGISTRATION NUMBER: 41,1
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amino acid
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IMMEDIATE SOURCE: CLONE: rl0n.pk0027.f11
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                                                                                                                                                                                                                                                                                                             APPLICANT: LIGHTNER,
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                       --KWWDIYN 292
                                                                                                                                                                                                                                                                                                                                                                                                                  DELAWARE
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                                                                                                                                                                                                506 HARWWKVYD 514
                                                                                                                                                                                                                                                                                       atent No. 6255114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            19898
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-073-297-14
                                                                                                                                                                                                                                                           US-09-073-297-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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  135
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199
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140 YAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYH
                 --FNSGVFVYQPSVETYN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVVKEIEPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDL
                                                       200 NLLETVKIVPPTLFAEQDFLNMYFK-----DIYKPIPPVYNLVLAMLWRHPENIEL--DQ
                                                                         -GEEENMDREDIKMLVKKWWDIYNDESLDYKNV
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                                                                                                                              Length 566;
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91;
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Pred. No. 1.5e-16
3; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                       . I. DU PONT DE NEMOURS AND MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
JRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                              APPLICANT: LIGHTNER, JONATHAN EDWARD TITLE OF INVENTION: STARCH BIOSYNTHETIC NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                   --LSAAPDP-GWPDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: BB-1083-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
FORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                     5, Application US/09073297
). 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/85261
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 22.3%; Pumatches 69; Conservative 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41,173
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LENGTH: 566 amino acids
                                                                                                                                                                                                 264
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PRIOR APPLICATION DATA:
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                                                                                                              VKVVHYCAAGAKPWRFT
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STREET: 1007 MARKE
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 302-7'
INFORMATION FOR SEQ
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MAPEINTKLTVPVHSATGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLP 60
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                    --SYPQLSAAGNNKVLFNSGVMVLEPS
                                                                                                                                                                         --GIHY--LGLKPWRCYRDYDCNWDLKTRRVYASESV
                                                                                                               -- VWWHRLSKRLNTM
                                                                                                                                                    -PENIELDQVKVVHYCAAGAKPWR-FTGEEENMDREDIKMLVK--
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                                                                        195 LSTYHNL-LETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: E. I. DU PONT DE NEMOURS AND COMPANY
F: 1007 MARKET STREET
WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                                   JONATHAN EDWARD STARCH BIOSYNTHETIC ENZYMES 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.4%; Score 225; DB 4. Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB-1083-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISM PC COMPATIBLE
                                                                                                 : :| |:: || ACLFEDLMLKSFKIGSYN-GGDQGFLNEYF
                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/09073297 Patent No. 6255114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41,173
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                                                                                                                                                                       | | | | : | 453 KYFGDESRHDKARNLPENLE--
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SEQUENCE CHARACTERISTICS:
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a

E: E. I. DU PONT DE NEMOURS AND COMPANY 1007 MARKET STREET

WILMINGTON DELAWARE

19898

SYSTEM: MICROSOFT WINDOWS 9' MICROSOFT WORD VERSION 7.0A

DISKETTE, 3.50 INCH

IBM PC COMPATIBLE

us/09/073,297

BB-1083-B

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TITLE OF INVENTION: STARCH BIOSYNTHETIC ENZYMES NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
RESULT 7
US-09-073-297-20
; Sequence 20, Application US/09073297
; Patent No. 6255114
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: MICROSO
                                                                                                                                                                       CITY: WI
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQ--GCVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                         STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113;
                                                                                                                                         , JONATHAN EDWARD
STARCH BIOSYNTHETIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 194; DB 4;
Pred. No. 2.7e-13
47; Mismatches 11:
                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MICROSOFT WINDOWS 9 SOFTWARE: MICROSOFT WORD VERSION 7.0A CURRENT APPLICATION DATA:
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----IGWPD---
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R: BB-1083-B
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FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                             Sequence 4, Application US/09073297 Patent No. 6255114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
FORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MAJARIAN, WILLIAM R
REGISTRATION NUMBER: 41,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
nilarity 22.6%;
Conservative 4
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amino acid
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                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                            LIGHTNER,
   TITLE OF INVENTION:
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MOLECULE TYPE:
S-09-073-297-4
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                                                                                                                                           APPLICANT:
                                                                              US-09-073-297-4
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Gaps
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                                                                                                                                                                      Length 43;
                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                      3 VTDPTPFAEQDFLNMFFRDVYKPIPPVYNLVLAMLWRNPRN 43
                                                                                                                                                                                                                                                                                                                                                                                                         JONATHAN EDWARD
STARCH BIOSYNTHETIC ENZYMES
26
                                                                                                                                                                                                                                       207 IVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAMLWRHPEN
                                                                                                                                                                    Score 187; DB 4;
Pred. No. 8.3e-14
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS DISKETTE, 3.50 INCH IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                      Sequence 16, Application US/09073297 Patent No. 6255114 GENERAL INFORMATION:
                                   not relevant
                                                                                                                                                                    Query Match
Best Local Similarity 78.0%;
Matches 32; Conservative
                                                              MOLECULE TYPE: peptide IMMEDIATE SOURCE: CLONE: wlml.pk0014.910
43 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1007 MARKET ST
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE,
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                         LIGHTNER,
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LIGHTNEI TITLE OF INVENTION:
                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: E. STREET: 1007 M
                                STRANDEDNESS:
                                                   TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                 US-09-073-297-20
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US-08-312-387B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFN 185
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                                  0;
48;
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STARCH BIOSYNTHETIC ENZYMES
26
                                                                                                                                                                                                                                                                                                                                                                                 Score 161; DB 4;
Pred. No. 3.7e-10;
7; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 AGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: MICROSOFT WINDOWS 95
MICROSOFT WORD VERSION 7.0A
SYSTEM: MICROSOFT WINDOWS 9' MICROSOFT WORD VERSION 7.0A
                                                                                                                                               41,173
SR: BB-1083-B
                                      US/09/073, 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08/852615
                                                                                        APPLICATION NUMBER: 08/852615
FILING DATE: MAY 7, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MAJARIAN, WILLIAM R.
                                                                                                                                        NAME: MAJANIEM, 173
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC COMPATIBLE YSTEM: MICROSOFT
                                                                                                                                                                                                                                                                                                                                                                                                           27;
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                                                                                                                                                                                                                    16:
                                                                                                                                                                                                                                                                          not relevant
                                                                                                                                                                                                                                                                                                                                                                                Match 8.9%;
Local Similarity 27.2%;
les 43; Conservative 2
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                                                                                                                                                                                                                                             amino acids
acid
                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                    TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: MAY 7,
                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: rrl.pk0070.e9-09-073-297-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: STANDER OF SEQUENCES: 2
                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: DISKETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGHTNER,
                                                                                                                                                                                                                                                                                        linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: E. 1007
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                                                                                                                                                                                                                                                                       STRANDEDNESS:
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STATE: DELL.
COUNTRY: U.(
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                                                     FILING DATE:
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  OPERATING
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             SOFTWARE:
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CITY: W1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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US-09-(
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21 KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVVKEI
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Patent No. 5545553
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
                                                                                                                                                                                                                                                                                                                                                                           Indels
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APPLICATION NUMBER: US/08/312,387B
FILING DATE: July 7, 1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                    Score 145.5; DB 4 Pred. No. 1.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNK 114
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                          BB-1083-B
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Klauber & Jackson
411 Hackensack Avenue
NAME: MAJARIAN, WILLIAM R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                        not relevant
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ilarity 34.0%;
Conservative 1
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LENGTH: 306 amino acids
TYPE: amino acid
                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: ctaln.pk0013.e6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SECTION CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hackensack
                                                                                                                                                                                                                                                                                                                                                         Similarity 32; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133521
                                                                                                                                                                                     STRANDEDNESS:
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STREET: 41
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US-08-312-387B-4
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Best Local
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59;
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CITY: H
STATE:
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Best Local
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                                                       ISHS 154
                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                     ----KIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK
                                                                                                                                                                                           DV - - MQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP
                                                                                                             --LETVK
                                                                                                                                                                                                                       287
                                                                                                                                                                                                                                                  293
                            68;
                                                    98 VINYSKLRIWEFV-EYNKMIYLDGDIQVFDNIDHLFDLPNGQFY--AVMDCFCEKTW
                                                                   AND GENES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
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                                                                                                                                                               207 IVPPTLFAEQDFLNMYFK------DIYKPIPPVYNLVL-AMLWRHPENIELDQ--
Length 306;
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
TITLE OF INVENTION: OLIGOSACCHARIDES, AND GENES ENCODING T
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 306;
                            Indels
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                                                                                                           PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
Score 134; DB 1;
Pred. No. 1.4e-06;
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25.0%; Pred. No. 1.4e-06;
ive 38; Mismatches 7.
                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, IRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Toward
                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08683426
Patent No. 5705367
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
                         38;
7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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USA
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             Similarity
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MOLECULE TYPE:
US-08-683-426-4
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                          59;
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                                                                                                                                                                                                                                                                                        RESULT 11
US-08-683-426-4
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Query Match
Best Local
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                                                                                                           155
                                                                                                                                                                                           181
                           Matches
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                                                                     -KIGMADGEYYFNAGVLLINLKKWRRHDIFKMSCEWVEQYK
                                     -LETVK
                                                                                                                                              181 DV -- MOYODODILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP
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Gotschlich, Emil C.
FENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF FONTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM SQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
                                                                                                                                                                                                        --DIKMLVKKW
ITTYARLKLGEYIADCDKVLYLDTDVLVRDGLKPLWDTDLGGNWVGACIDLFVER-
                                                                                                           -DIYKPIPPVYNLVL-AMLWRHPENIELDQ-
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                                    PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71;
                                                                                                                                                                                  --RFT---GEEENMDRE----
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1.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
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APPLICATION NUMBER: US/08/683,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible (YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/312,387
FILING DATE: September 26, 1994
                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08683458
Patent No. 5798233
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klauber & Jackson
Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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LENGTH: 306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                           207 IVPPTLFAEQDFLNMYFK-
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: GL
TITLE OF INVENTION: OL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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MOLECULE TYPE:
8-683-458-4
                                                                       ---QEGYKQ-
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252
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                           181 DV -- MQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANGFASRHTDPLYLDRTNTAMP
                                                                                   293
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                                                                                                                                                                                                   Gotschlich, Emil C.
FOUTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS OF FOUTION: OLIGOSACCHARIDES, AND GENES ENCODING THEM SQUENCES: 12
                                                                         -DIKMLVKKW
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 ---DIYKPIPPVYNLVL-AMLWRHPENIELDQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1
                                                         --RFT---GEEENMDRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            600-1-095B
                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/878,360
18-JUN-1997
N: 435
                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/312,387
er 26, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08/683,426
                                                                                                                                                                                                                                                                          Klauber & Jackson
Hackensack Avenue
                                                                                                                                                          Sequence 4, Application US/08878360
Patent No. 5945322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: September 26, CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TOR APPLICATION DATA:
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TITLE OF INVENTION: OL
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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    IVPPTLFAEQDFLNMYFK
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FILING DATE: 18-JUN
                                                                                                                                                                                                                                                                           Klauber
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                                                                                                                                                                                                                                                                                                                       New Jersey
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                                                         VKVVHYCAAGAKPW
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Best Local Similarity
Watches 59; Conser
                                                                                                                                                                       Patent No. 5945322
GENERAL INFORMATION:
APPLICANT: Gotsch
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US-08-878-360-4
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                                                                                                                                       STEPHEN
LA, STEPHANIE L.
N: METHOD OF TRANSFERRING AT LEAST TWO
N: SACCHARIDE UNITS WITH A POLYGLYCOSYLTRANSFERASE,
N: POLYGLYCOSYLTRANSFERASE AND GENE ENCODING A
N: POLYGLYCOSYLTRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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              --DIYKPIPPVYNLVL-AMLWRHPENIELDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 306;
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                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
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Pred. No. 1.4e-06;
-GEEENWDRE
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                                                                                                                                                                                                                                                        1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                    Sequence 4, Application US/08478140B Patent No. 6127153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (212) 790-9090
(212) 869-9741/8864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
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N: 435
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                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 amino acids
amino acid
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APPLICATION NUMBER: US,
FILING DATE: 07-JUN-19
                                                                                                                             KARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                    ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                   BUCZALA,
                                                                                                                                                                            OF INVENTION:
                                                                                                                             JOHNSON,
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 VKVVHYCAAGAKPW
                                                                                                                                                                                                                   NUMBER OF SEQUENCES
                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                   New York
                                                                                                  atent No. 6127153
GENERAL INFORMATION
APPLICANT: JOHNS
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                         ROTH,
                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66141
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                                                                                                                                                                                                                                                                                               USA
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                                                               RESULT 14
US-08-478-140B-4
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APPLICANT:
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       S-U9-333-412-4
Sequence 4, Application US/09333412
Patent No. 6342382
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gotschlich, Emil C.
APPLICANT: Gotschlich, Emil C.
TITLE OF INVENTION: GLYCOSYLTRANSFERASES FOR BIOSYNTHESIS
OLIGOSACCHARIDES, AND GENES ENCODING 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68;
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                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQYKIGYCQQCPDKVTWPEAKLG-PKPPLYFNAGMFVYEPNLSTYHNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 7.4%; Score 134; DB 4; I Similarity 25.0%; Pred. No. 1.4e-06; 59; Conservative 38; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/312,387
FILING DATE: July 7, 1994
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-095
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----RFT---GEEENMDRE-
                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/333,412
FILING DATE: 15-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-333-412-4
                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 306 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                   ZIP: 07601
COMPUTER READABLE FORM:
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US-09-333-412-4
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12:08:57 2002, 7 July Search completed: Job time: 174 sec

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version
- 2000
GenCore (c) 1993
      Copyright
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using sw model - protein search, OM protein

) l updates/sec Search time 53.7 Seconds (without alignments) 692.918 Million cell 2002, 12:08:26; 7 July Run on:

US-09-810-506-2 Title:

1816 score: Perfect

Sequence:

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Gapext • BLOSUM62 Gapop 10.0 Scoring table:

0.5

747574 seqs, 111073796 residues Searched:

747574 hits satisfying chosen parameters of Total number

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*
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| SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT:*

RESULT

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No and is score

SUMMARIES

		Description	S Arabidopsis thalia	Arabidopsis	Arabidopsis								
		ID	AAG14525	AAG4574	AAG14526	AAG45748	AAR31580	AAR31581	AAW82560	AAE05241	AAG14527	AAG45749	AAB72462
		DB	21	21	21	21	14	14	19	22	21	21	22
		h Length DB	344	344	333	333	330	328	328	328	279	279	117
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265.5 265.5 265.5 248 241 241 241 224 227 227 227 227 227 227 227 227 227	9 4 4 4 4 6
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ALIGNMENTS

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Arabidopsis thaliana protein fragment SEQ ID NO: 14420
               344 AA.
               standard; Protein;
                                                                       entry)
                                                                     (first
                                                                      17-OCT-2000
                                          AAG14525;
             AAG14525
AAG14525
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pathway; promoter; metabolic por control; p Protein identification; signal transduction pathway; nhybridisation assay; genetic mapping; gene expression termination sequence.

Arabidopsis thaliana

EP1033405-A2

06-SEP-2000

99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128714.. 99US-0130479. 2000EP-0301439 25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 16-APR-1999; 16-APR-1999; 16-APR-1999; 25-FEB-2000;

9US-0130819 9US-013089 9US-013144 9US-013240 9US-013248 9US-013248 9US-013248 9US-013286 9US-013421 9US-013421 9US-013421	99US-0134941. 99US-0135124. 99US-0135124. 99US-0135629. 99US-0136021. 99US-013722. 99US-013722. 99US-0137528. 99US-0137528. 99US-013864. 99US-0139452. 99US-0139452. 99US-0139455. 99US-0139455. 99US-0139455.	905-013946 905-013946 905-013946 905-013975 905-013989 905-013989 905-014082 905-014082 905-014128 905-014128	9US-014239 9US-014280 9US-014297 9US-014354 9US-014362 9US-014408 9US-014408 9US-014433 9US-014433 9US-014433
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25 - FEB - 1999; 05 - MAR - 1999; 25 - MAR - 1999; 26 - MAR - 1999; 27 - MAR - 1999; 28 - MAR - 1999; 28 - MAR - 1999; 29 - MAY - 1999; 21 - APR - 1999; 21 - APR - 1999; 22 - MAY - 1999; 23 - APR - 1999; 24 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - APR - 1999; 28 - APR - 1999; 29 - MAY - 1999; 29 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 21 - MAY - 1999; 22 - MAY - 1999; 23 - APR - 1999; 24 - MAY - 1999; 25 - MAY - 1999; 26 - MAY - 1999; 27 - MAY - 1999; 28 - JUN - 1999; 29 - JUN - 1999; 29 - JUN - 1999; 29 - JUN - 1999; 20 - JUN - 1999; 20 - JUL - 1999; 20 - J
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est Local Similarity 74.7%;
atches 257; Conservative
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Mismatches
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99US-0156596.

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99US-0159294.

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99US-0159330.

99US-0159331.

99US-0159638.

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99US-0159638.

99US-0160741.

99US-0160981.

99US-0160981.

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99US-0161404.

99US-0161404.

99US-0161360.

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ilarity 74.7%;
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29-SEP-1999;
05-OCT-1999;
06-OCT-1999;
07-OCT-1999;
13-OCT-1999;
13-OCT-1999;
14-OCT-1999;
14-OCT-1999;
14-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
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22-OCT-1999;
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fragment
protein
thaliana
Arabidopsis
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

thaliana Arabidopsis

EP1033405-A2

-2000 -SEP-90

2000EP-0301439 -FEB-2000; 25

99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126264.
99US-0126264.
99US-0126264.
99US-0128714.
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99US-0139455. 25-FEB-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 25-MAR-1999; 01-APR-1999; 06-APR-1999; 06-APR-1999; 16-APR-1999; 16-APR-1999; 17-APR-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 18-MAY-1999; 19-MAY-1999; 14-MAY-1999; 16-MAY-1999; 17-MAY-1999; 18-MAY-1999; 18-MAY-1999; 19-MAY-1999; 10-JUN-1999; 16-JUN-1999; 18-JUN-1999; 18-JUN-1999;

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RR 22-JUN-1999 RR 23-JUN-1999 RR 23-JUN-19999 RR 28-JUN-19999 RR 29-JUN-19999 RR 29-JUN-19999 RR 01-JUL-19999 RR 009-JUL-19999 RR 13-JUL-19999 RR 13-JUL-19999 RR 13-JUL-19999 RR 15-JUL-19999 RR 19-JUL-19999 RR 19-JUL-19999 RR 19-JUL-19999 RR 20-JUL-19999 RR 20-JUL-19999	PR 21-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 23-JUL-1999; PR 27-JUL-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 20-AUG-1999; PR 27-AUG-1999;

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Pred. No. 9.9e
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9905-0151303.
9905-0151438.
9905-0151930.
9905-0152363.
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9905-0154039.
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Query Match
Best Local S
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Dy 306 Valvalkefitalteagrinytapsaa 333

NESUTA

Add45748 standard; Protein; 333 AA.

Add45748 standard; Protein; Add444.

PROTEIN; Protei
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Pred. No. 9.9e
0; Mismatches
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99US-0149368.
99US-0149426.
99US-0149426.
99US-0149723.
99US-0149723.
99US-0149929.
99US-0149929.
99US-0149930.
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99US-0158333.
99US-0158333.
99US-0159330.
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99US-0159838.
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99US-0159339.
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Local Similarity 77.4%
Les 254; Conservative
16-AUG-1999;

18 -AUG-1999;

20 -AUG-1999;

20 -AUG-1999;

20 -AUG-1999;

20 -AUG-1999;

21 -AUG-1999;

22 -AUG-1999;

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25 -AUG-1999;

26 -AUG-1999;

27 -AUG-1999;

27 -AUG-1999;

28 -SEP-1999;

29 -SEP-1999;

21 -OCT-1999;

22 -SEP-1999;

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24 -SEP-1999;

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26 -OCT-1999;

27 -AUG-1999;

28 -SEP-1999;

29 -SEP-1999;

21 -OCT-19999;

21 -OCT-19999;

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                                                          and
                                                                                                                                                                                                                                                                                                                                                                                CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                             Galactinol synthase; enzyme; raffinose saccharide; sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of galactinol synthase from zucchini ssoybean - used to produce plants having altered levels of raffinose saccharide(s) and/or sucrose
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                                                                                                                                                                                                                                                                                                                                                                                synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Pages 59-61; 80pp; English.
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                                                                                                                                                                                  KKQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                                                                                                  306 vdlvnlkpfitalteagrlnyvtapsaa
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N-PSDB; AAQ36503.
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Schweiger BJ;
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VHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKNVVIGDSHKKQQTLQQ
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                                                                                                                                                                                                                                                                                                                                                                           enzyme; raffinose saccharide; sucrose
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levels of
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Pred. No. 2.7e-137;
9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of galactinol synthase from soybean - used to produce plants having altered raffinose saccharide(s) and/or sucrose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61-63; 80pp; English
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llarity 74.3%;
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                                                                                                                                                                                                                                                                                                                               entry)
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311 lvsvlseaevvnhitapsaa
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                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max Cultivar Wye.
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N-PSDB; AAQ36504.
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Best Local Similarity
Matches 251; Conser
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Gaps

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Indels

Score 1360.5; DB 14; Pred. No. 1.3e-137; 36; Mismatches 41; I

Query Match
Best Local Similarity 75.6%;
Matches 242; Conservative

Length 330

7ggc

12

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16

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This sequence represents a rice glycogenin-like water stress proteins. Which is used in a method to isolate novel plant glycogenin proteins. Such proteins can be used to alter plant glycogenin and water stress protein expression. Manipulation of glycogenin expression can be used to alter starch biosynthesis and effects the number of starch granules in the endosperm of corn. Overexpression or reduction of expression of genes encoding glycogenin in corn, rice and wheat could be used to alter branch chain distribution of the starch produced by these plants
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skmiy
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plvva
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|vynlv
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                                             Q,
                                                                                                                                                         PKPPLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPP
MAPEINT-KLTVPVHSA--TGGEKRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKY
           LDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                 corn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to alter
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-nvdkftaalmevgevkfvrapsaa
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                                                                                                                                                                                                                                                                                                                                                                                                         stress protein.
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                                                                                                                                                                                                                                                                                                                                 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                  entry)
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                     Gaps
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                                                         PLYFNAGMFVYEPNLSTYHNLLETVKIVPPTLFAEQDFLNMYFKDIYKPIPPVYNLVLAM
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water s
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                    8;
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                     Indels
         Pred. No. 3.8e-133;
; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glycogenin; water stress-induced property transgenic plant; plant breeding
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                                                                                                                                                                                                                                                                                              VVIGDSHKKQQTLQQFIEALSEAGALQYVKAPSAA
                                                                                                                                                                                                                                                                                                                                                                                    AAE05241 standard; Protein; 328 AA
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71.08; Fr. 41;
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                      Conservative
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          1 Similarity
238; Conser
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            Best Local
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is present at higher or lower levels than normal or in cell types or developmental stages in which it is not normally found. The nucleic acid fragments are also used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to expression of a corn, rice and wheat glycogenin or water stress protein. The cDNAs of the invention are used in plant breeding to develop cell lines with desired starch phenotypes. The antibodies of glycogenin or water stress proteins are used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.
                                                                                                                                                                                                                                                                                                                                                                                                                  pathway;
promoter;
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                                                                                                                                                                                                                                                                LWRHPENIELDQVKVVHYCAAGAKPWRFTGEEENMDREDIKMLVKKWWDIYNDESLDYKN
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                                                                                                                                                                                                                                                                                                                                                                                                            riocein identification; signal transduction pathway; metabolic
hybridisation assay; genetic mapping; gene expression control;
termination sequence.
                                                                                                                        α
                                                                                                       Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                   thaliana protein fragment SEQ ID NO: 14422
                                                                                                      72.6%; Score 1319; DB 22;
llarity 71.0%; Pred. No. 3.8e-133;
Conservative 41; Mismatches 48;
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0126785.
99US-0127462.
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238; Conser
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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PR 16-APR-1999; 99US-0129845.

PR 23-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130077.

PR 23-APR-1999; 99US-0130049.

PR 28-APR-1999; 99US-0130891.

PR 28-APR-1999; 99US-013248.

PR 30-APR-1999; 99US-013248.

PR 05-MAY-1999; 99US-013248.

PR 10-MAY-1999; 99US-013248.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 15-MAY-1999; 99US-0134219.

PR 16-MAY-1999; 99US-0134219.

PR 16-MAY-1999; 99US-013445.

PR 16-MAY-1999; 99US-013345.

PR 16-MAY-1999; 99US-013345.

PR 16-MAY-1999; 99US-013345.

PR 16-MAY-1999; 99US-013345.

PR 18-MAY-1999; 99US-013345.

PR 23-MAY-1999; 99US-013345.

PR 23-MAY-1999;
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PR 19-JUL-1999; 99US-0144334.

PR 20-JUL-1999; 99US-0144834.

PR 20-JUL-1999; 99US-0144834.

PR 21-JUL-1999; 99US-0146834.

PR 22-JUL-1999; 99US-0146834.

PR 22-JUL-1999; 99US-0146086.

PR 22-JUL-1999; 99US-0145086.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145087.

PR 23-JUL-1999; 99US-0145087.

PR 02-AUG-1999; 99US-0145087.

PR 02-AUG-1999; 99US-014508.

PR 02-AUG-1999; 99US-01440.2.

PR 03-AUG-1999; 99US-01440.2.

PR 03-AUG-1999; 99US-01440.2.

PR 13-AUG-1999; 99US-014508.

PR 13-AUG-1999; 99US-015508.

PR 13
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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-123;
31;
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Pred. No. 7.3e-1
}; Mismatches
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99US-0159329.
99US-0159331.
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99US-0159638.
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99US-0160741.
99US-0160767.
99US-0160814.
99US-0160980.
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99US-0161404.
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9; Conservative
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14 -OCT - 1999;
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Matches 219;
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                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                                                 Score 1222.5; DB 2:
Pred. No. 7.3e-123;
; Mismatches 31;
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990S-0157117.
990S-015753.
990S-0158029.
990S-0158232.
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990S-0159293.
990S-0159294.
990S-0159295.
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990S-0160980.
990S-0160980.
990S-0160981.
990S-0160981.
990S-0161405.
990S-0161405.
990S-0161359.
990S-0161359.
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Local Similarity 78.5%
es 219; Conservative
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04-0CT-1999;
06-0CT-1999;
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08-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
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14-0CT-1999;
21-0CT-1999;
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Matches 219
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The present invention relates to a method for determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity. The method comprises exposing an acceptor substrate for UGGT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful in glucosyltransferase assay and kinetics measurement for determining UGGT activity. UGGT is a soluble enzyme of the endoplasmic reticulum which catalyses the addition of a glucose residue onto asparagine-linked oligosaccharides, which are present on incorrectly folded glycoproteins. The present sequence was used in a sequence homology comparison with rat UGGT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 FVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFYAVMDCFCEKTWSHSPQYKIGYCQQCPDK 168
                                                                                                                                                                                             Determining the effect of a test sample on UDP-glucose:glycoprotein glucosyltransferase (UGGT), useful for measuring UGGT activity, comprises exposing an acceptor substrate for UGGT to a labeled donor the presence of UGGT -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Partial sequence, no start codon given"
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Pred. No. 3.2e-45;
3; Mismatches 19
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                                                                                                                                                  JJM,
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                                                                                                                                                   Bergeron
                                                                                                                                                                                                                                                                           Disclosure; Fig 10; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                         CANADA
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illarity 72.6%;
Conservative 1:
                                                                  2000WO-CA00883
                                                                                             99US-0376330
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                                                                                                                        RES COUNCIL
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85; Conserv
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             WO200112845-A1.
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DC
                                       22-FEB-2001
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Matches
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                                                                                                                                                      This sequence represents a novel corn glycogeniu procession alters plant cc3.mn0001.f7. This protein is used in a method which alters plant glycogenin and water stress protein expression. Manipulation of glycogenin expression can be used to alter starch biosynthesis and effects the number of starch granules in the endosperm of corn. Overexpression or reduction of expression of genes encoding glycogenin in corn, rice and wheat could be used to alter branch chain distribution of the starch produced by these plants.
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                                                                                                         Plant glycogenin and water stress proteins - used to alter pla glycogenin and water stress protein expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 starch biosy
                                                                                                                                                                                                                                                                            Length 346;
                                                                                                                                                                                                                                                                                                                   KRAYVTFLAGTGDYVKGVVGLAKGLRKAKSKYPLVVAVLPDVPEDHRKQLVDQGCVV
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                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                            Score 265.5;
Pred. No. 1.3
                                                                                                                                      57pp; English.
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27.6%;
                   97US-0852615
98WO-US09201
                                       (DUPO ) DU PONT DE NEMOURS
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                                                                                                                                                                                                                                                                                               Conservative
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transgenic plant; plant
                                                                                                                                      Claim la; Page 27-28;
                                                                             1998-610384/51
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                               346 AA;
                                                                                     N-PSDB; AAV69345
                  07-MAY-1997;
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06-MAY-1998;
                                                          Lightner JE;
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Best Local
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The present sequence is corn glycogenin protein from cc3.mn0001.f7 clone.

The present invention relates to plant glycogenin or water stress

proteins and their corresponding nucleic acid sequences. Glycogenin
is a self-glucosylating protein involved in the synthesis of glycogen

Which plays a major role in starch biosynthesis. Over-expression

Treduction of glycogenin gene expression alters the branch chain

are used to isolate cDNAs and genes encoding homologous glycogenins and
water stress proteins from the same or other plant species, or to create

transgenic plants in which an instant glycogenin or water stress protein

spresent at higher or lower levels than normal or in cell types or

developmental stages in which it is not normally found. The nucleic acid

the genes that they are a part of, and as markers for traits linked to

expression of a corn, rice and wheat glycogenin or water stress protein.

The cDNAs of the invention are used in plant breeding to develop cell

lines with desired starch phenotypes. The antibodies of glycogenin or
water stress proteins are used to screen cDNA expression libraries to

scalate full-length cDNA clones of interest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 EPVYPPENQTEFAMAYYVINYSKLRIWEFVEYNKMIYLDGDIQVFDNIDHLFDLPNGQFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 AVMDCFCEKTWSHSPQYKIGYCQQCPDKVTWPEAKLGPKPPLYFNAGMFVYEPNLSTYHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---fnsgvmviepsnctfrl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VVHYCAAGAKPWR-FTGEEENMDREDIKMLVK-----KWWDIYN
                                                                                                                                                                                                                                                                               New glycogenin polynucleotides and polypeptides or water proteins, useful for encoding homologous glycogenins and proteins from the same or other plant species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                 97US-0852615
  98US-0073297
                                                                                                   (DUPO ) DU PONT DE NEMOURS
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                                                                                                                                                       Everard JD;
                                                                                                                                                                                                     WPI; 2001-432051/46.
N-PSDB; AAD09245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 AA;
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                                                                                                                                                    Lightner JE,
06-MAY-1998;
                                              07-MAY-1997;
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
15-APR-1999;
16-APR-1999;
16-APR-1999;
16-APR-1999;
17-APR-1999;
18-APR-1999;
19-APR-1999;
19-APR-1999;
10-APR-1999;
11-MAY-1999;
11-APR-1999;
11-APR-1999;
11-AUN-1999;
                                                                                                 EP1033405-A2
                                                                                                                                 25-FEB-2000;
                                Arabidopsis
                                                                                Arabidopsis
                                                                                                                06-SEP-2000
                 18-OCT-2000
AAG39868;
 13
                                                                                                                                                                                                                                                is
                                                                                                                                                                                        or more cell-cell
                                                                                                                                                                                                                                                                                                                from WIPO
                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
(ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPC at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                               119
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                 insecticide;
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and
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                                                                                                                                                                                                                       Sequence Listing;
                 signalling;
 20130
                                                                                                                                                                                                                                                                                                                                                                                94;
                                                                                                                                                                                        detection reagent for for elucidating cell
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Pred. No. 7.1e-18;
4; Mismatches 94
 ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --lsaapd-vswpdc-
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                cell
polypeptide SEQ
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               biology;
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25.7%;
                                                                                                       2000US-191637P
2000US-0614150
                                                                                        2001WO-US09231
                                                                                                                                                                                       New isolated nucleic acid
genes from Drosophila and
interactions -
                 developmental
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 Drosophila melanogaster
                                        melanogaster
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                                                                                                                                                               2001-656860/75
                                                                                                                                X
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Best Local Similarity
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                                                        WO200171042-A2
                       pharmaceutical
                                                                                        23-MAR-2001;
                                                                                                       23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                       Disclosure;
                                                                        27-SEP-2001
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                                        Drosophila
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                 Drosophila
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pathway;
promoter;
                                           Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence.
                       49390
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                        SEO
                        fragment
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99US-0123180.
99US-0123180.
99US-0123548.
99US-0126264.
99US-0126264.
99US-0126264.
99US-0126264.
99US-0128234.
99US-0132487.
99US-0133622.
99US-0135529.
99US-0135629.
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99US-0137528.
99US-0139425.
99US-0139455.
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                      thaliana protein
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9US-0139463 9US-0139750 9US-0139763 9US-0139817 9US-0140353 9US-0140695 9US-0140695 9US-0140695 9US-0141287 9US-0141287	990S-0142154. 990S-0142390. 990S-0142803. 990S-0142803. 990S-0143624. 990S-0144005. 990S-0144085. 990S-0144332. 990S-0144333. 990S-0144332. 990S-0144332. 990S-0144332. 990S-0144884. 990S-0144884. 990S-0145086.	90S-0145089 90S-0145145 90S-0145145 90S-0145218 90S-0145224 90S-0145913 90S-0145919 90S-0145918 90S-0145918 90S-0145919 90S-0145951 90S-0146386 90S-0146386 90S-0146389 90S-0147302	9US-0147303 9US-0147416 9US-0147493 9US-0147935 9US-0148341 9US-0148341 9US-0148684 9US-0149426 9US-0149426 9US-0149723 9US-0149929 9US-01499029
18-JUN-1999 18-JUN-1999 21-JUN-1999 22-JUN-1999 23-JUN-1999 24-JUN-1999 24-JUN-1999 29-JUN-1999 30-JUN-1999 01-JUL-1999 01-JUL-1999	22-700 22-700 23-700 23-700 23-700 20-700	22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 02-AUG-1999 02-AUG-1999 02-AUG-1999 03-AUG-1999 04-AUG-1999 05-AUG-1999	R 06-AUG-1999 R 06-AUG-1999 R 09-AUG-1999 R 10-AUG-1999 R 11-AUG-1999 R 13-AUG-1999 R 13-AUG-1999 R 13-AUG-1999 R 20-AUG-1999 R 20-AUG-1999 R 23-AUG-1999

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                                                                                                                                                                                                                                                                                                                                                                                                       108;
                                                                                                                                                                                                                                                                                                                                                                                         Length 614;
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lwqltdydkiifidadllilrnidflfsmpeisatgnngtl
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Pred. No. 2e-17;
3; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                       53;
990S-0150884.
990S-0151065.
990S-0151066.
990S-0151080.
990S-0151303.
990S-0151333.
990S-0151333.
990S-0151339.
990S-0151339.
990S-0158029.
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990S-0159293.
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990S-0159638.
990S-0159638.
990S-0160981.
990S-0160981.
990S-0160981.
990S-0161404.
990S-0161406.
990S-0161359.
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Best Local Similarity 24.3%;
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      KLTVPVHS
26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
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Qy	219	219 LNMYFKDIYKPIPPVYNLVLAMLWRHPENIELDQVKVVHYCAAGAKPWR 267
QQ	434	434 lnevftwwhr-ipkhmnf-lkhfwigdeddakrkktelfgaeppvlyvlhylgmkpwl 489
Qy	268) ESLDYKNVVIGDSHKKQ
qq	490	490 cyrdydcnfnsdifvefatdiahrkwwmvhdampqelhqfcylrs 534
Qy	322	322 EAGA-LQYVKAPSAA 335
QΩ	535	i I i i i i i i i i i i i i i i i i i i
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